

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:24:52 ; Search time 25 Seconds
(without alignments)
1672.139 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEFRLKAGALGKLM.....YGATHSTFQPRPPPPVRYD 560

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2970	100.0	560	1 US-08-647-484-2	Sequence 2, Appl1
2	2970	100.0	560	1 US-08-647-481-2	Sequence 2, Appl1
3	2970	100.0	560	1 US-08-430-033A-2	Sequence 2, Appl1
4	2970	100.0	560	5 PCT-US96-05792-2	Sequence 2, Appl1
5	2962	99.7	567	4 US-09-949-016-11354	Sequence 1, Appl1
6	2925	98.5	560	2 US-08-805-118-4	Sequence 4, Appl1
7	2925	98.5	560	4 US-09-391-958-4	Sequence 4, Appl1
8	2925	98.5	560	4 US-09-915-181A-5	Sequence 5, Appl1
9	2313.5	77.9	578	4 US-09-740-041-7	Sequence 4, Appl1
10	2313.5	77.9	582	4 US-09-915-181A-4	Sequence 4, Appl1
11	2185	73.6	589	4 US-09-740-041-2	Sequence 2, Appl1
12	2174.5	73.2	850	4 US-09-915-181A-3	Sequence 3, Appl1
13	1297	43.7	576	3 US-08-864-785-1	Sequence 1, Appl1
14	1294	43.6	563	4 US-09-915-181A-6	Sequence 6, Appl1
15	940	31.6	495	4 US-09-359-167-2	Sequence 2, Appl1
16	940	31.6	495	4 US-09-915-181A-7	Sequence 7, Appl1
17	940	31.6	536	4 US-09-359-167-8	Sequence 8, Appl1
18	940	31.6	585	4 US-09-949-016-7705	Sequence 7705, Ap
19	931	31.3	495	4 US-09-359-167-4	Sequence 4, Appl1
20	746	25.1	552	4 US-09-270-767-45540	Sequence 45540, A
21	673	22.7	497	4 US-09-949-016-6616	Sequence 6616, Ap
22	636.5	21.4	495	4 US-09-359-167-12	Sequence 12, Appl
23	636.5	21.4	495	4 US-09-359-167-12	Sequence 12, Appl
24	626.5	21.1	467	2 US-08-805-118-3	Sequence 3, Appl1
25	626.5	21.1	467	2 US-09-391-958-3	Sequence 9, Appl1
26	620	20.9	480	2 US-08-724-394A-9	Sequence 8, Appl1
27	615	20.7	465	4 US-09-915-181A-8	

28	487.5	16.4	436	4 US-09-949-016-11448	Sequence 11448, A
29	483.5	16.3	470	2 US-08-724-394A-10	Sequence 10, Appl
30	479	16.1	401	2 US-08-805-118-1	Sequence 1, Appl1
31	479	16.1	401	3 US-09-391-958-1	Sequence 1, Appl1
32	476.5	16.0	480	2 US-08-724-394A-11	Sequence 11, Appl
33	428.5	14.4	460	4 US-09-489-039A-9663	Sequence 9663, Ap
34	416.5	14.0	380	4 US-09-949-016-7053	Sequence 7053, Ap
35	385.5	13.0	470	4 US-09-328-352-6912	Sequence 6912, Ap
36	378.5	12.7	455	4 US-09-489-039A-9942	Sequence 9942, Ap
37	367.5	12.4	163	4 US-09-270-767-32926	Sequence 32926, A
38	367.5	12.4	163	4 US-09-270-767-48143	Sequence 48143, A
39	345	11.6	443	4 US-09-489-039A-9335	Sequence 9335, Ap
40	330.5	11.1	444	4 US-09-492-709A-258	Sequence 258, App
41	322.5	10.9	234	4 US-09-270-767-45527	Sequence 45527, A
42	322.5	10.9	434	4 US-09-489-039A-13633	Sequence 13633, A
43	321.5	10.8	442	4 US-09-489-039A-12384	Sequence 12384, A
44	316	10.6	459	4 US-09-489-039A-10630	Sequence 10630, A
45	309	10.4	451	4 US-09-489-039A-7269	Sequence 7269, Ap

ALIGNMENTS

RESULT 1
US-08-647-484-2
; Sequence 2, Application US/08647484
; Patent No. 5618677
; GENERAL INFORMATION:
; APPLICANT: NI, Binhui
; TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
; TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/647,484
; FILING DATE: 14-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/430,033
; FILING DATE: 27-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-647-484-2
Query Match 100.0%; Score 2970; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.8e-278; Indels 0; Gaps 0;
Matches 560; Conservative 0; Mismatches 0;
1 MEFRQEFRLKAGALGKLMLEKROGAETTLASDGRPVTTQTRDPVVDCTCFGLP 60
|||||

Db 1 MEPROEERFKLAGRALGKHLRLERKQBAETLEISADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVOQAQPSMDPEVGLIH 120
Db 61 RRYIIAIMGSGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 121 GSFPMGYIVTOIPGFIQCKFPAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILQG 180
Db 121 GSFPMGYIVTOIPGFIQCKFPAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILQG 180
QY 181 LVEGTYTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
Db 181 LVEGTYTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
QY 241 YGSFGIFWYLFMLVLYSYPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPMRRFPT 300
Db 241 YGSFGIFWYLFMLVLYSYPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPMRRFPT 300
QY 301 SMPVVAIIYANFCRSMTFYLLISQPDYFEEVFGFISKVGIVSALPHLWMTIIVPIGQ 360
Db 301 SMPVVAIIYANFCRSMTFYLLISQPDYFEEVFGFISKVGIVSALPHLWMTIIVPIGQ 360
QY 361 IADPLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSKGVASFLVLAVGSGFATS 420
Db 361 IADPLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSKGVASFLVLAVGSGFATS 420
QY 421 GENVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIVGAMTKKTRREMOYVFLIASLVHY 480
Db 421 GENVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIVGAMTKKTRREMOYVFLIASLVHY 480
QY 481 GGVIYGVFASGEKQPMAPPEEMSEKCGFVGHDLAGSDSEMEDAEAPPGAPAPAPPS 540
Db 481 GGVIYGVFASGEKQPMAPPEEMSEKCGFVGHDLAGSDSEMEDAEAPPGAPAPAPPS 540
QY 541 YGATHSTQPPRRPPVVDY 560
Db 541 YGATHSTQPPRRPPVVDY 560

RESULT 2
US-08-647-481-2
Sequence 2, Application US/08647481
Patent No. 5618918
GENERAL INFORMATION:
APPLICANT: Nt, Binhui
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,481
FILING DATE: 14-MAY-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,033
FILING DATE: 27-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10006
TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-647-481-2

Query Match 100.0%; Score 2970; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.8e-278;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPROEERFKLAGRALGKHLRLERKQBAETLEISADGRPVTTQTRDPVVDCTCFGLP 60
Db 1 MEPROEERFKLAGRALGKHLRLERKQBAETLEISADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVOQAQPSMDPEVGLIH 120
Db 61 RRYIIAIMGSGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 121 GSFPMGYIVTOIPGFIQCKFPAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILQG 180
Db 121 GSFPMGYIVTOIPGFIQCKFPAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILQG 180
QY 181 LVEGTYTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
Db 181 LVEGTYTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
QY 241 YGSFGIFWYLFMLVLYSYPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPMRRFPT 300
Db 241 YGSFGIFWYLFMLVLYSYPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPMRRFPT 300
QY 301 SMPVVAIIYANFCRSMTFYLLISQPDYFEEVFGFISKVGIVSALPHLWMTIIVPIGQ 360
Db 301 SMPVVAIIYANFCRSMTFYLLISQPDYFEEVFGFISKVGIVSALPHLWMTIIVPIGQ 360
QY 421 GENVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIVGAMTKKTRREMOYVFLIASLVHY 480
Db 421 GENVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIVGAMTKKTRREMOYVFLIASLVHY 480
QY 481 GGVIYGVFASGEKQPMAPPEEMSEKCGFVGHDLAGSDSEMEDAEAPPGAPAPAPPS 540
Db 481 GGVIYGVFASGEKQPMAPPEEMSEKCGFVGHDLAGSDSEMEDAEAPPGAPAPAPPS 540
QY 541 YGATHSTQPPRRPPVVDY 560
Db 541 YGATHSTQPPRRPPVVDY 560

RESULT 3
US-08-430-033A-2
Sequence 2, Application US/08430033A
Patent No. 5686266
GENERAL INFORMATION:
APPLICANT: Nt, Binhui
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/430.033A
 APPLICATION NUMBER: US/08/430.033A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gaylo, Paul J.
 REGISTRATION NUMBER: 36,808
 REFERENCE/DOCKET NUMBER: X-10006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 276-0756
 TELEFAX: (317) 276-3861
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 560 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-430-033A-2

Query Match 100.0%; Score 2970; DB 1; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.8e-278;
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFROEERKLAGALGKLRLEKROGAELELSADGRVTTQTRDPVVDCTCFGLP 60
 DB 1 MEFROEERKLAGALGKLRLEKROGAELELSADGRVTTQTRDPVVDCTCFGLP 60
 QY 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGHVVOXQFSDPBTGILH 120
 DB 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGHVVOXQFSDPBTGILH 120
 QY 121 GSPFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLIPSAARVHYGCVIFVRILOG 180
 DB 121 GSPFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLIPSAARVHYGCVIFVRILOG 180
 QY 181 LVEGVTPACHGIVSKAPPLERSRLATTACGSYAGAVVAMPPLAGVIVQYSGMSVYV 240
 DB 181 LVEGVTPACHGIVSKAPPLERSRLATTACGSYAGAVVAMPPLAGVIVQYSGMSVYV 240
 QY 241 YGSGFIEMVLFMWLVSYSPALHPSISEERKYLEDAIGESAKMNPITKSTPARRRFT 300
 DB 241 YGSGFIEMVLFMWLVSYSPALHPSISEERKYLEDAIGESAKMNPITKSTPARRRFT 300
 QY 301 SMPVYAIIVANFCGSMWTFYLLISQPDYFEEVFGEISKGLVSLPHLVMTIIVPIGQ 360
 DB 301 SMPVYAIIVANFCGSMWTFYLLISQPDYFEEVFGEISKGLVSLPHLVMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVKRLNCGGFGMEATLLVVGYSKGVASFLVLAVGSGFAIS 420
 DB 361 IADFLRSRIMSTNVKRLNCGGFGMEATLLVVGYSKGVASFLVLAVGSGFAIS 420
 QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITVGMATGKTRKREMOYVFLIASLVHY 480
 DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITVGMATGKTRKREMOYVFLIASLVHY 480
 QY 481 GGVIFYGVFASGEKOPMAPEEMSEKCGFVGHDLAASDDSEMEDEAPGAPAPPPS 540
 DB 481 GGVIFYGVFASGEKOPMAPEEMSEKCGFVGHDLAASDDSEMEDEAPGAPAPPPS 540
 QY 541 YGATHSTFQPPRPVVDY 560
 DB 541 YGATHSTFQPPRPVVDY 560

RESULT 4
 PCT-US96-05792-2
 Sequence 2, Application PC/TUS9605792
 GENERAL INFORMATION:
 APPLICANT: Ni, Binhui

APPLICANT: Paul, Steven M.
 TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
 TITLE OF INVENTION: PHOSPHATE COTRANSPORTER
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Eli Lilly and Company
 STREET: Lilly Corporate Center
 CITY: Indianapolis
 STATE: Indiana
 COUNTRY: United States of America
 ZIP: 46285
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/05792
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/430.033
 FILING DATE: April 27, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Gaylo, Paul J.
 REGISTRATION NUMBER: 36,808
 REFERENCE/DOCKET NUMBER: X-10006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (317) 276-0756
 TELEFAX: (317) 276-3861
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 560 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US96-05792-2

Query Match 100.0%; Score 2970; DB 5; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.8e-278;
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFROEERKLAGALGKLRLEKROGAELELSADGRVTTQTRDPVVDCTCFGLP 60
 DB 1 MEFROEERKLAGALGKLRLEKROGAELELSADGRVTTQTRDPVVDCTCFGLP 60
 QY 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGHVVOXQFSDPBTGILH 120
 DB 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGHVVOXQFSDPBTGILH 120
 QY 121 GSPFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLIPSAARVHYGCVIFVRILOG 180
 DB 121 GSPFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLIPSAARVHYGCVIFVRILOG 180
 QY 181 LVEGVTPACHGIVSKAPPLERSRLATTACGSYAGAVVAMPPLAGVIVQYSGMSVYV 240
 DB 181 LVEGVTPACHGIVSKAPPLERSRLATTACGSYAGAVVAMPPLAGVIVQYSGMSVYV 240
 QY 241 YGSGFIEMVLFMWLVSYSPALHPSISEERKYLEDAIGESAKMNPITKSTPARRRFT 300
 DB 241 YGSGFIEMVLFMWLVSYSPALHPSISEERKYLEDAIGESAKMNPITKSTPARRRFT 300
 QY 301 SMPVYAIIVANFCGSMWTFYLLISQPDYFEEVFGEISKGLVSLPHLVMTIIVPIGQ 360
 DB 301 SMPVYAIIVANFCGSMWTFYLLISQPDYFEEVFGEISKGLVSLPHLVMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVKRLNCGGFGMEATLLVVGYSKGVASFLVLAVGSGFAIS 420
 DB 361 IADFLRSRIMSTNVKRLNCGGFGMEATLLVVGYSKGVASFLVLAVGSGFAIS 420
 QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITVGMATGKTRKREMOYVFLIASLVHY 480
 DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITVGMATGKTRKREMOYVFLIASLVHY 480

QY 481 GGVIYGVASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPPPS 540
DB 481 GGVIYGVASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPPPS 540
QY 541 YGATHSTFQPPRPVPPVRY 560
DB 541 YGATHSTFQPPRPVPPVRY 560

RESULT 5

US-09-949-016-11354
; Sequence 11354, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11354
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11354

Query Match 99.7%; Score 2962; DB 4; Length 567;
Best Local Similarity 99.8%; Pred. No. 1.1e-277;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFRQEEPRKLAGRALGKHLRLLEKROGAEITLISADGRPVTTOTRDPVVDCTCGFLP 60
DB 8 MEFRQEEPRKLAGRALGKHLRLLEKROGAEITLISADGRPVTTOTRDPVVDCTCGFLP 67
QY 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSTTHRGHVVOKAQFMDPEVGLIH 120
DB 68 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSTTHRGHVVOKAQFMDPEVGLIH 127
QY 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRILQG 180
DB 128 GSFPMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRILQG 187
QY 181 LVEGVTYPACGHWKMAPPLERSRLATTAFGSGYAGAVVAMPPLAGVLVQSGMSVFYV 240
DB 188 LVEGVTYPACGHWKMAPPLERSRLATTAFGSGYAGAVVAMPPLAGVLVQSGMSVFYV 247
QY 241 YGSFGIFWYLFMLVLYSESPALHPSISEBERKXIIEAIGESAKLMLPTKFTPMRPF 300
DB 248 YGSFGIFWYLFMLVLYSESPALHPSISEBERKXIIEAIGESAKLMLPTKFTPMRPF 307
QY 301 SMPVYAIIVANPCRSWTFYLLISQPDYEEVFGFEISKVGLVSALPHLVMITIIYVIGQ 360
DB 308 SMPVYAIIVANPCRSWTFYLLISQPDYEEVFGFEISKVGLVSALPHLVMITIIYVIGQ 367
QY 361 IADPLRSRIMSTNVKRLMNCGGFMEATLLLVYVSHSKVAISFLVLAVGSGFALS 420
DB 368 IADPLRSRIMSTNVKRLMNCGGFMEATLLLVYVSHSKVAISFLVLAVGSGFALS 427
QY 421 GENVHLIDAPRYASITMGISNGVGTLSGWCPIIVGAMTKKTRBEMQYVELIASLVHY 480
DB 428 GENVHLIDAPRYASITMGISNGVGTLSGWCPIIVGAMTKKTRBEMQYVELIASLVHY 487
QY 481 GGVIYGVASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPPPS 540

DB 488 GGVIYGVASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPPPS 547
QY 541 YGATHSTFQPPRPVPPVRY 560
DB 548 YGATHSTFQPPRPVPPVRY 567

RESULT 6

US-08-805-118-4
; Sequence 4, Application US/08805118
; Patent No. 5985604
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
; TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,118
; FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0221 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 507415
US-08-805-118-4

Query Match 98.5%; Score 2925; DB 2; Length 560;
Best Local Similarity 98.2%; Pred. No. 4.1e-274;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEFRQEEPRKLAGRALGKHLRLLEKROGAEITLISADGRPVTTOTRDPVVDCTCGFLP 60
DB 1 MEFRQEEPRKLAGRALGKHLRLLEKROGAEITLISADGRPVTTOTRDPVVDCTCGFLP 60
QY 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSTTHRGHVVOKAQFMDPEVGLIH 120
DB 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSTTHRGHVVOKAQFMDPEVGLIH 120
QY 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRILQG 180
DB 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRILQG 180
QY 181 LVEGVTYPACGHWKMAPPLERSRLATTAFGSGYAGAVVAMPPLAGVLVQSGMSVFYV 240
DB 181 LVEGVTYPACGHWKMAPPLERSRLATTAFGSGYAGAVVAMPPLAGVLVQSGMSVFYV 240

QY 241 YGSGFIEMYLFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTKSTPWRPFT 300
 Db 241 YGSGFIEMYLFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTKSTPWRPFT 300
 QY 301 SMPYVAIIIVANPCRSWTFYLLISQPDYFEEVFGFEISKVGLVSLPHLVMTIIVPIGQ 360
 Db 301 SMPYVAIIIVANPCRSWTFYLLISQPDYFEEVFGFEISKVGLVSLPHLVMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVRKLMNCGGFGMEATLLLVGYSHSKGVALISFLVLAVGSGFAIS 420
 Db 361 IADFLRSRIMSTNVRKLMNCGGFGMEATLLLVGYSHSKGVALISFLVLAVGSGFAIS 420
 QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITIVGAMTKHKTREEMQYVFLASLVHY 480
 Db 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITIVGAMTKHKTREEMQYVFLASLVHY 480
 QY 481 GGVIIFYGVFASGEKQPMAPPEMSEKCGFVGHQDLASDSEMEDAEPPGAPPAPPS 540
 Db 481 GGVIIFYGVFASGEKQPMAPPEMSEKCGFVGHQDLASDSEMEDAEPPGAPPAPPS 540
 QY 541 YGATHSTVQPPRPPPPVADY 560
 Db 541 YGATHSTVQPPRPPPPVADY 560

RESULT 7

US-09-391-958-4
 ; Sequence 4, Application US/09391958
 ; Patent No. 6326207
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Bandman, Olga
 ; TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
 ; TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Discrete
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/391,958
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/805,118
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0221 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 560 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 507415
 ; US-09-391-958-4

Query Match 98.5%; Score 2925; DB 3; Length 560;
 Best Local Similarity 98.2%; Pred. No. 4,16-274;
 Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEPROEERKLAGALGKRLHLEKROGAETLELSADGRVTTQTDRPPVDDCTCFGLP 60
 Db 1 MEPROEERKLAGALGKRLHLEKROGAETLELSADGRVTTQTDRPPVDDCTCFGLP 60
 QY 61 RRYIIAMSGLGFICISGIRCNLGVAVLSMVNNSSTRGGHVVYQKQFMDPETVGLIH 120
 Db 61 RRYIIAMSGLGFICISGIRCNLGVAVLSMVNNSSTRGGHVVYQKQFMDPETVGLIH 120
 QY 121 GSFFMGYIVTQIPGFIQKRAANRVGFALVATSTNMLIPSAARVHYGCVIFVRILQG 180
 Db 121 GSFFMGYIVTQIPGFIQKRAANRVGFALVATSTNMLIPSAARVHYGCVIFVRILQG 180
 QY 181 LVEGVTPACHGINSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVQYSGMSVRYV 240
 Db 181 LVEGVTPACHGINSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVQYSGMSVRYV 240
 QY 241 YGSGFIEMYLFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTKSTPWRPFT 300
 Db 241 YGSGFIEMYLFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTKSTPWRPFT 300
 QY 301 SMPYVAIIIVANPCRSWTFYLLISQPDYFEEVFGFEISKVGLVSLPHLVMTIIVPIGQ 360
 Db 301 SMPYVAIIIVANPCRSWTFYLLISQPDYFEEVFGFEISKVGLVSLPHLVMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVRKLMNCGGFGMEATLLLVGYSHSKGVALISFLVLAVGSGFAIS 420
 Db 361 IADFLRSRIMSTNVRKLMNCGGFGMEATLLLVGYSHSKGVALISFLVLAVGSGFAIS 420
 QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITIVGAMTKHKTREEMQYVFLASLVHY 480
 Db 421 GFNNHLDIAPRYASILMGISNGVGTLSGMVCPITIVGAMTKHKTREEMQYVFLASLVHY 480
 QY 481 GGVIIFYGVFASGEKQPMAPPEMSEKCGFVGHQDLASDSEMEDAEPPGAPPAPPS 540
 Db 481 GGVIIFYGVFASGEKQPMAPPEMSEKCGFVGHQDLASDSEMEDAEPPGAPPAPPS 540
 QY 541 YGATHSTVQPPRPPPPVADY 560
 Db 541 YGATHSTVQPPRPPPPVADY 560

RESULT 8

US-09-915-181A-5
 ; Sequence 5, Application US/09915181A
 ; Patent No. 6818391
 ; GENERAL INFORMATION:
 ; APPLICANT: EDWARDS, ROBERT
 ; APPLICANT: BELLOCCHIO, ELIZABETH
 ; APPLICANT: FREMEAUX, ROBERT
 ; APPLICANT: REIMER, RICHARD
 ; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
 ; FILE REFERENCE: 305T-932610US
 ; CURRENT APPLICATION NUMBER: US/09/915,181A
 ; CURRENT FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: US 60/220,556
 ; PRIOR FILING DATE: 2000-07-25
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Rattus rattus
 ; US-09-915-181A-5

Query Match 98.5%; Score 2925; DB 4; Length 560;
 Best Local Similarity 98.2%; Pred. No. 4,16-274;
 Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MEPROEERKLAGALGKRLHLEKROGAETLELSADGRVTTQTDRPPVDDCTCFGLP 60

```
Db 1 MEFROEERKLAGRALGRHLRLEKKEQEAETLELSADRPVYTHTRDPVVDCTCFGLP 60
Qy 61 RRYIYIIMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGVYVQAKQSPMBETVGLH 120
Db 61 RRYIYIIMSGLGFCISFGIRCNLGVAVISMVNNSTTHRGVYVQAKQSPMBETVGLH 120
Qy 121 GSEFMWGYIVTOIPGGFICQKFAANRVFGAIVATSTLNLIPSAARVHVCVIFVAILGQ 180
Db 121 GSEFMWGYIVTOIPGGFICQKFAANRVFGAIVATSTLNLIPSAARVHVCVIFVAILGQ 180
Qy 181 LVEGVTYPAACHGWSKMAPPLERSRLATTAFCGSYAGAVAMPPLAGVLVOYSGMSVFV 240
Db 181 LVEGVTYPAACHGWSKMAPPLERSRLATTAFCGSYAGAVAMPPLAGVLVOYSGMSVFV 240
Qy 241 YGSFGIFWTLFVNLVYESPALHPSISEBERKXIEDAIGESAKLNPPLTKFSTPMRPF 300
Db 241 YGSFGIFWTLFVNLVYESPALHPSISEBERKXIEDAIGESAKLNPPLTKFSTPMRPF 300
Qy 301 SMPVYAIIVANFCRSWTFYLLISQPDYEEVGFESIKVGLVSALPHLWMTIIVBIGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLISQPDYEEVGFESIKVGLVSALPHLWMTIIVBIGQ 360
Qy 361 IADPLRSRIMSTNTRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAIS 420
Db 361 IADPLRSRIMSTNTRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAIS 420
Qy 421 GRNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGANTKHKTRBEMQVFLIASLVH 480
Db 421 GRNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGANTKHKTRBEMQVFLIASLVH 480
Qy 481 GGVIYFVAFASGEKQWAPPEMSEBEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
Db 481 GGVIYFVAFASGEKQWAPPEMSEBEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
Qy 541 YGATHSTFOPPPPPPPVRY 560
Db 541 YGATHSTFOPPPPPPPVRY 560

RESULT 9
US-09-740-041-4
; Sequence 4, Application US/09740041
; Patent No. 6562593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-740-041-4

Query Match 77.9%; Score 2313.5; DB 4; Length 578;
Best Local Similarity 79.3%; Pred. No. 6,3e-215;
Matches 428; Conservative 57; Mismatches 50; Indels 5; Gaps 2;
```

```
Db 132 WGYITVTOIPGGFIQKFAANRVFGAIVATSTLNLIPSAARVHVCVIFVAILGQVVG 191
Qy 185 VTYPAACHGWSKMAPPLERSRLATTAFCGSYAGAVAMPPLAGVLVOYSGMSVFVYGSF 244
Db 192 VTYPAACHGWSKMAPPLERSRLATTAFCGSYAGAVAMPPLAGVLVOYSGMSVFVYGSF 251
Qy 245 GIFWTLFVNLVYESPALHPSISEBERKXIEDAIGESAKLNPPLTKFSTPMRPF 304
Db 252 GNVWTFVNLVYESPALHPSISEBERKXIEDAIGESAKLNPPLTKFSTPMRPF 311
Qy 305 YAIIVANFCRSWTFYLLISQPDYEEVGFESIKVGLVSALPHLWMTIIVBIGQIDF 364
Db 312 YAIIVANFCRSWTFYLLISQPDYEEVGFESIKVGLVSALPHLWMTIIVBIGQIDF 371
Qy 365 IASRIMSTNTRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAISGFV 424
Db 372 IASRIMSTNTRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAISGFV 431
Qy 425 NHLDIAPRYASILMGISNGVGLSGMVCPIIVGANTKHKTRBEMQVFLIASLVH 484
Db 432 NHLDIAPRYASILMGISNGVGLSGMVCPIIVGANTKHKTRBEMQVFLIASLVH 491
Qy 485 FYGVAFASGEKQWAPPEMSEBEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPSYAT 544
Db 492 FYGVAFASGEKQWAPPEMSEBEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPSYAT 546

RESULT 10
US-09-915-181A-4
; Sequence 4, Application US/09915181A
; Patent No. 6818391
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMBAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-915-181A-4

Query Match 77.9%; Score 2313.5; DB 4; Length 582;
Best Local Similarity 79.3%; Pred. No. 6,4e-215;
Matches 428; Conservative 57; Mismatches 50; Indels 5; Gaps 2;
```

Db 253 GMMVMEFWLVSYESPAKHPTTDEERRRYIESIGESANLLGAMKEFKTPMRKEFTSNPV 312
Qy 305 YAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIGGQINDF 364
Db 313 YAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIGGQINDF 372
Qy 365 LRSRRIMSTTVKRLMNCGFGMEATLLLVGYSHSKVAISFLVAVGFGFPAISGFNV 424
Db 373 LRSQIISTTVKRLMNCGFGMEATLLLVGYSHTRVVALSFLVAVGFGFPAISGFNV 432
Qy 425 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVHYGVI 484
Db 433 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVHYGVI 492
Qy 485 FYGVFASGEKQPMABPEEMSEKGFVGHDLGSDSEMDABPPCAPAPPSPYCAT 544
Db 493 FYALFASGEKQPMADPEETSEKGFIDEHL---DETDGDIQ-NYINYGTTSYGAT 547

RESULT 11
US-09-740-041-2
; Sequence 2, Application US/09740041
; Patent No. 6562593
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO01001
; CURRENT APPLICATION NUMBER: US/09/740, 041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Human
US-09-740-041-2

Query Match 73.6%; Score 2185; DB 4; Length 589;
Best Local Similarity 76.3%; Pred. No. 1.8e-202;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

Qy 5 QEEFRKLGRALGKHLRLERKRGAEITLISADGRPVTTQTRDPVVDCTCFGLPRRYI 64
Db 18 KEGVKNAVDSLGILQKIDGTTEEDNIEINSEGRPVQTSRPAVDCDCGCPKRYI 77
Qy 65 IAINSGIGFCISFGIRCNLGAIVSMVNSSTTHRGHVVOAKQFSDPETVGLHGSFF 124
Db 78 IAINSGIGFCISFGIRCNLGAIVEMVNSSTVYDGRKEIQTAQFNDPETVGLHGSFF 137
Qy 125 WGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMILPSARVHYGCVIFVRILQGLEG 184
Db 138 WGYIMTQIPGGFICQKFAANRVFGFAIVATSTLNMILPSARVHYGCVIFVRILQGLEG 197
Qy 185 VTYACGIGWSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFPVYGSF 244
Db 198 VTYACGIGWSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFPVYGSF 257
Qy 245 GIFYWLEFWLVSYESPALPHSISEBERKTIEDALIGSALKMPLTKFSTPMRRFETSMVP 304
Db 258 GIIVYMFLLQAYECPAHPTISNEKTYIETISIGEGANVVS-LSKFSTPMKRPTSLIPV 316
Qy 305 YAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIGGQINDF 364
Db 317 YAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIGGQINDF 376
Qy 365 LRSRRIMSTTVKRLMNCGFGMEATLLLVGYSHSKVAISFLVAVGFGFPAISGFNV 424
Db 377 LRSQIISTTVKRLMNCGFGMEATLLLVGYSHSKVAISFLVAVGFGFPAISGFNV 436
Qy 425 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVHYGVI 484

Db 437 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVHYGVI 496
Qy 485 FYGVFASGEKQPMABPEEMSEKGFVGHDLGSDSEMDABPPCAPAPPSPYCAT 544
Db 497 FYGVFASGEKQPMADPEETSEKGGIIDDDELA--ETELNHES--FASFKKMSYGAT 551

RESULT 12
US-09-915-181A-3
; Sequence 3, Application US/09915181A
; Patent No. 6818391
; GENERAL INFORMATION:
; APPLICANT: EDMARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAUX, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-93261005
; CURRENT APPLICATION NUMBER: US/09/915, 181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-3

Query Match 73.2%; Score 2174.5; DB 4; Length 850;
Best Local Similarity 76.0%; Pred. No. 3.2e-201;
Matches 414; Conservative 51; Mismatches 69; Indels 11; Gaps 5;

Qy 5 QEEFRKLGRALGKHLRLERKRGAEITLISADGRPVTTQTRDPVVDCTCFGLPRRYI 64
Db 26 KEGVKNAVDSLGILQKIDGTTEEDNIEINSEGRPVQTSRPAVDCDCGCPKRYI 85
Qy 65 IAINSGIGFCISFGIRCNLGAIVSMVNSSTTHRGHVVOAKQFSDPETVGLHGSFF 120
Db 86 IAINSGIGFCISFGIRCNLGAIVEMVNSSTVYDGRKEIQTAQFNDPETVGLHGSFF 145
Qy 121 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMILPSARVHYGCVIFVRILQ 180
Db 146 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMILPSARVHYGCVIFVRILQ 205
Qy 181 LVEGVTPACGIGWSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFPVY 240
Db 206 LVEGVTPACGIGWSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYSGMSVFPVY 265
Qy 241 YGSFGITFWYLFMLIV-SYESPALHPSISEBERKTIEDALIGSALKMPLTKFSTPMRRF 299
Db 266 YGMFGIITWYMFLLQAYECPAHPTISNEKTYIETISIGEGANVVS-LSKFSTPMRRF 324
Qy 300 TSMFVYAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIG 359
Db 325 TSMFVYAIIVANCRSWTFFLLISQDPYEEVGFGEISKVGLVSAALPHLVMTIIVPIG 384
Qy 360 QIADFLRSRRIMSTTVKRLMNCGFGMEATLLLVGYSHSKVAISFLVAVGFGFPAI 419
Db 385 QIADFLRSRRIMSTTVKRLMNCGFGMEATLLLVGYSHSKVAISFLVAVGFGFPAI 444
Qy 420 SGRVNHLDIAPRYSILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVH 479
Db 445 SGRVNHLDIAPRYSILMGISNGVGLSGMVCPIIVGAMTKHKTREEMQVYELIALSVH 504
Qy 480 YGVIFYGVFASGEKQPMABPEEMSEKGFVGHDLGSDSEMDABPPCAPAPPSPYCAT 539
Db 505 YGVIFYGVFASGEKQPMADPEETSEKGGIIDDDELA--ETELNHES--FASFKKMSYGAT 559
Qy 540 SYGAT 544
Db 560 SYGAT 564

```
RESULT 13
; US-08-864-785-1
; Sequence 1, Application US/08864785A
; Patent No. 6329566
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Joshua M.
; APPLICANT: Oppenheimer, Allison J.
; APPLICANT: Hart, Anne C.
; TITLE OF INVENTION: METHODS FOR THE DETECTION, TREATMENT,
; FILE OF INVENTION: AND PREVENTION OF NEURODEGENERATION
; FILE REFERENCE: 00786/353001
; CURRENT APPLICATION NUMBER: US/08/864,785A
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 576
; TYPE: PR
; ORGANISM: Caenorhabditis elegans
US-08-864-785-1
```

```
Query Match 43.7%; Score 1297; DB 3; Length 576;
Best Local Similarity 47.7%; Pred. No. 1.4e-116;
Matches 262; Conservative 88; Mismatches 171; Indels 28; Gaps 10;

QY 9 RKLGRALGKHLRLLEKQGEAETLELSADGRVTTQTDRD---PVVDCGCGFLPR-RYIA 64
DB 12 KQVGEPLKMTAAASATGAAPPOQOEENENPMQHSNKVLQVMEQWTIGCKRKL 71
QY 65 IAIMSGAFCSIFGIRCNLGVAVSMVNSSTHGGHVVVOKAQSMDPEVGLIHGSF 124
DB 72 LAIIANMGWMSIFGIRCNFGAATKTHMYKNTDYG---KVHMEFNTIDELSWESSYF 128
QY 125 NGYIVTQIGGFCQGFANRVFGPAIVATSTMLIPSAARYHG-CVIFRILQGLVE 183
DB 129 YGLVLTQIPAGFLAAKFPENKLFSGIGVGAFLNILLPYGFKVSDYLAFTQITGLVQ 188
QY 184 GATYVPCGHISWAPLEERSRLATTAFCGSYAGAVVAMPVLAAGLVQYSGWSPVYVGS 243
DB 189 GACYPAMGVWRYWAPPMERSKLTATTAFTGSYAGAVLGLPLSAFLVSVMAPFLYLV 248
QY 244 FGIFWYFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTFSTPMRRFTSNP 303
DB 249 CGYVAILMPCVTFEKPAPHPTISQEKIFIEDAIGHVN-THPTIR-SIPWKAIVTSKP 306
QY 304 VYAIIVANCRSWTFYLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGQIAD 363
DB 307 VVAIIIVANFARSWTFYLLQNLTYMKKALGKMIADSGLLAAIPIHLMGCVLMGQIAD 366
QY 364 FLRSRIMSTNVRKLMNCGGFGMEATLLVGYSHSKGVAISFLVLAAGSGFAISGN 423
DB 367 YRSNKILSTTAVRKIFNCGFGGEBAFMLIVAYTISDTTAIMALIAAVGSGFAISGN 426
QY 424 VNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHREMOYVFLIASLVHYGV 483
DB 427 VNHLDIAPRYAIIIMGFSNGIGTLAGLTCPTVEATTAH-SKHGWSVFLIASLIHFTV 485
QY 484 IYGVFASGEKQPAEPEENSE-----EKCGFVG-----HDQLAGSDSEMEDE 527
DB 486 TEYAVVYASGELQEWAPKEEENSKELVNTKGTINGYGALETFTQLPAGVDSYQAQ 545
QY 528 AEP-PGAPP 535
DB 546 AAPAGTNP 554
```

```
RESULT 14
; US-09-915-181A-6
; Sequence 6, Application US/09915181A
; Patent No. 6818391
; GENERAL INFORMATION:
```

```
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAUX, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 563
; TYPE: PR
; ORGANISM: Caenorhabditis elegans
US-09-915-181A-6
```

```
Query Match 43.6%; Score 1294; DB 4; Length 563;
Best Local Similarity 47.9%; Pred. No. 2.7e-116;
Matches 262; Conservative 86; Mismatches 171; Indels 28; Gaps 10;

QY 11 IAGRLGKHLRLLEKQGEAETLELSADGRVTTQTDRD---PVVDCGCGFLPR-RYIA 66
DB 1 NVGEPLAKMTAAASATGAAPPOQOEENENPMQHSNKVLQVMEQWTIGCKRKLIA 60
QY 67 IAIMSGAFCSIFGIRCNLGVAVSMVNSSTHGGHVVVOKAQSMDPEVGLIHGSF 126
DB 61 IIANMGWMSIFGIRCNFGAATKTHMYKNTDYG---KVHMEFNTIDELSWESSYF 117
QY 127 YIVTQIPGFCQGFANRVFGPAIVATSTMLIPSAARYHG-CVIFRILQGLVEG 185
DB 118 YVLTQIPAGFLAAKFPENKLFSGIGVGAFLNILLPYGFKVSDYLAFTQITGLVQ 177
QY 186 TYPACHGISWAPLEERSRLATTAFCGSYAGAVVAMPVLAAGLVQYSGWSPVYVGS 245
DB 178 CYPAMGVWRYWAPPMERSKLTATTAFTGSYAGAVLGLPLSAFLVSVMAPFLYLV 237
QY 246 IFWYFWLLVSYESPALHPSISEERKXIEDAIGESAKLMNPLTFSTPMRRFTSNP 305
DB 238 VTMALMPCVTFEKPAPHPTISQEKIFIEDAIGHVN-THPTIR-SIPWKAIVTSKP 295
QY 306 AIIVANFCRSWTFYLLISQPDYEEVFGFEISKVGLVSALPHLVMTIIVPIGQIAD 365
DB 296 AIIVANFARSWTFYLLQNLTYMKKALGKMIADSGLLAAIPIHLMGCVLMGQIAD 355
QY 366 RSRIMSTNVRKLMNCGGFGMEATLLVGYSHSKGVAISFLVLAAGSGFAISGN 425
DB 356 RSNKILSTTAVRKIFNCGFGGEBAFMLIVAYTISDTTAIMALIAAVGSGFAISGN 415
QY 426 HDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHREMOYVFLIASLVHYGV 485
DB 416 HDIAPRYAIIIMGFSNGIGTLAGLTCPTVEATTAH-SKHGWSVFLIASLIHFTV 474
QY 486 YGVFASGEKQPAEPEENSE-----EKCGFVG-----HDQLAGSDSEMEDE 529
DB 475 YAVVYASGELQEWAPKEEENSKELVNTKGTINGYGALETFTQLPAGVDSYQAQ 534
QY 530 P-PGAPP 535
DB 535 PAPGNTNP 541
```

```
RESULT 15
; US-09-359-167-2
; Sequence 2, Application US/09359167
; Patent No. 6803448
; GENERAL INFORMATION:
; APPLICANT: Hellerqvist, Carl
; APPLICANT: Fu, Changlin
; TITLE OF INVENTION: GBS Toxin Receptor
; FILE REFERENCE: CARB-008/01US
; CURRENT APPLICATION NUMBER: US/09/359,167
```



```

; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 60-693,843
; EARLIER FILING DATE: 1998-07-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-359-167-2

```

```

Query Match      31.6%  Score 940; DB 4; Length 495;
Best Local Similarity 39.5%  Pred. No. 4e-82;
Matches 193; Conservative 93; Mismatches 162; Indels 40; Gaps 8;

```

```

QY 38 DGRPTTQTRDPVVDCTCFGLPR-----RYIAIMSGLGFCISFGIRCNLGVAI 87
DB 12 DGEESTDRT---PLLP---GAPRAEAPVCCSARYNLALIAFFGFPIVYALRVNLVYAL 64
QY 88 VSMVNNSTT-----HRGHHVVVQKQ---FSMDPEYVGLHGSFPMGYIVYQI 132
DB 65 VDMWDSNTTLEDNRTSKACPEHSAPIKVHNNOTGKKYQMDAETQWILGSFFYGIITQI 124
QY 133 PGGFICQFAANRVGFAIVATSTLMMLPSAARVHVCVIFVRILOGLVEGVTPACHG 192
DB 125 PGYVASKIGGKMLGFGILGTAULTFTPIADLGVGPLIVLRALBGLGEGVTFPAMHA 184
QY 193 IWSKAPPLERSRLATTAFCCSYAGAVVAMPILAGVLVOYSGWSSVFYVYGSFGLFWYLF 252
DB 185 MMSMWAPPLERSKLLISYAGAQOLGTVISLPLSGIICYMMWTVYFFFGTIGIFWFLM 244
QY 253 LLVYESPALHPSTISEERKXIEDAIGESAKLMNPL-TKFTSPMRFFFTSMPPVYAIIVAN 311
DB 245 IWLVSDFQKHRIKISHYEKEYI-----LSSLRNQLSQKSVPMVPIKLSLPLMAIVAH 298
QY 312 FCRSMTFYLLISQDYFEEVGFELISKVGLVSAALPHLMTIIVPIGGQIADFLSRRIIM 371
DB 299 FSYMTFTYLLTLPTWKELIRFVQENGFLSSLPYLGSWLCHLISGQADNLRKKNP 358
QY 372 STTVRKLMNCCGFGMEATLLVVGY-SHSKGVASFLVLAVGFSGPAISGFNNHLDIA 430
DB 359 STLCVRRIFSLIGMIGPAVFLVAGFICDYSLAVAFLLISTYLGFCSSGFSINHLDA 418
QY 431 PRVASIIMGISNGVGLSCMCPILVGMTHKTRREMOYFELIASLVHYGVIFYGVA 490
DB 419 PSYAGILGINTNTPTATIPGMVGPVIAKSLTDPNTVGENQTVFYIAAALNVGALFTLLFA 478
QY 491 SGEKQPMNA 498
DB 479 KGEVQNMNA 486

```

```

Search completed: June 2, 2005, 11:32:55
Job time : 27 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:28:43 ; Search time 56 Seconds
(without alignments)
1150.617 Million cell updates/sec

Title: US-10-734-731-4

Perfect score: 2970

Sequence: 1 MEFRQEEFRKLAGRALGKLM.....YGATHSTRQPPRPVVDY 560

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 546557 seqs, 115061664 residues

Total number of hits satisfying chosen parameters: 546557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Pending Patents AA New:*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1198.5	40.4	US-11-097-143-4995	Sequence 4995, Ap
2	986.5	33.2	US-11-097-143-8367	Sequence 8367, Ap
3	986.5	33.2	US-11-097-143-24411	Sequence 24411, A
4	927	31.2	US-60-655-875-146571	Sequence 146571, A
5	798	26.9	US-11-097-143-2895	Sequence 2895, Ap
6	769.5	25.9	US-11-097-143-27831	Sequence 27831, A
7	767.5	25.8	US-11-097-143-17844	Sequence 17844, A
8	747	25.2	US-11-097-143-5532	Sequence 5532, Ap
9	726	24.4	US-60-669-241-28729	Sequence 28729, A
10	719.5	24.2	US-11-097-143-11013	Sequence 11013, A
11	716.5	24.1	US-11-097-143-20922	Sequence 20922, A
12	708	23.8	US-60-669-175-21828	Sequence 21828, A
13	699.5	23.6	US-11-097-143-28257	Sequence 28257, A
14	698.5	23.6	US-11-097-143-37224	Sequence 37224, A
15	698.5	23.5	US-11-097-143-9567	Sequence 9567, Ap
16	695.5	23.4	US-11-097-143-21597	Sequence 21597, A
17	693.5	23.4	US-11-097-143-15315	Sequence 15315, A
18	692	23.3	US-60-669-175-22572	Sequence 22572, A
19	685.5	23.1	US-11-097-143-37218	Sequence 37218, A
20	676	22.8	US-11-097-143-37221	Sequence 37221, A
21	671	22.6	US-11-097-143-19404	Sequence 19404, A
22	644.5	21.7	US-11-097-143-6948	Sequence 6948, Ap
23	616	20.7	PCT-US05-11532-1919	Sequence 1919, Ap
24	616	20.7	PCT-US05-11532-1920	Sequence 1920, Ap
25	615	20.7	US-11-097-143-20859	Sequence 20859, A

26	596.5	20.1	449	7	US-11-097-143-2769	Sequence 2769, Ap
27	595.5	20.1	313	8	US-60-669-175-28254	Sequence 28254, A
28	577	19.4	468	7	US-11-097-143-17484	Sequence 17484, A
29	558	18.8	444	7	US-11-097-143-20862	Sequence 20862, A
30	557	18.8	492	7	US-11-097-143-3039	Sequence 3039, Ap
31	496	16.7	473	7	US-11-097-143-6987	Sequence 6987, Ap
32	483	16.3	401	6	US-10-938-061-113	Sequence 113, App
33	483	16.3	401	6	US-10-938-626-113	Sequence 113, App
34	481	16.2	379	6	US-10-531-176-18	Sequence 18, App1
35	477	16.1	420	6	US-10-938-061-112	Sequence 112, App
36	477	16.1	420	6	US-10-938-626-112	Sequence 112, App
37	469.5	15.8	452	8	US-60-669-175-23389	Sequence 23389, A
38	468.5	15.8	307	6	US-10-450-763-43033	Sequence 43033, A
39	434	14.6	614	6	US-10-450-763-52553	Sequence 52553, A
40	433	14.6	246	8	US-60-669-175-35181	Sequence 35181, A
41	433	14.6	287	8	US-60-669-175-21944	Sequence 21944, A
42	426.5	14.4	309	8	US-60-669-175-27828	Sequence 27828, A
43	415.5	14.0	439	7	US-11-097-143-38628	Sequence 38628, A
44	412	13.9	247	8	US-60-669-241-27469	Sequence 27469, A
45	386.5	13.0	438	7	US-11-043-889-55	Sequence 55, App1

ALIGNMENTS

```
RESULT 1
US-11-097-143-4995
; Sequence 4995, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4995
; LENGTH: 560
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-4995
Query Match 40.4%; Score 1198.5; DB 7; Length 560;
Best Local Similarity 46.8%; Pred. No. 5.2e-88;
Matches 244; Conservative 70; Mismatches 144; Indels 63; Gaps 11;
```

QY 38 DGRPT-----TQTDPPV-----VDCTFGLPRTYIAIMSGLCGFCISFGIRCNIGV 85
DB 61 DRRDPSRPSFEIRFPKDKCKACPC--MPARTITMACVGMIFGRCKNMSA 118
QY 86 AIVSMVNNSTTRGHGVVQKQPSWDPEYVGLIHGSFWMGYIVTQIPGFIQCKEAFNR 145
DB 119 AKLGEHNGYTF-----MMWTVAVBSHYDSSPFMGVLTQIRGFIASKFPANK 167

[illegible]

```

RESULT 2
US-11-097-143-8367
; Sequence 8367, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8367
; LENGTH: 502
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-8367

```

Query Match	33.2%	Score 986.5	DB 7	length 502
Best Local Similarity	38.0%	Pred. No. 4,8-71		
Matches	200	Conservative	96	Mismatches 185; Indels 45; Gaps 7
Qy	13	GRATGKRLLEKROGCAETLELSADGEPVTTQTRDPVVDCTCGLPRTYIATMSG	72	
	10	IKHLIEQVA-----ONNTEIT-----SEPLTW-----FWRKQRYIVVLLAFEG	48	
Db				

```

QY 7 FCI$FICRNL$VALIV$WNN$STH$RGHV$VQ$A$Q$M$P$E$T$G$L$H$G$F$M$G$Y$T$Q$L 132
Db 49 F$V$V$Y$L$R$N$L$S$V$A$L$V$M$T$E$N$R$Y$T$D$A$G$N$V$Y$Q$D$F$M$B$K$Q$G$L$L$S$F$F$G$Y$L$T$Q$F 108
QY 133 P$G$F$I$C$Q$E$P$A$N$V$F$G$A$L$V$A$T$S$T$N$M$L$I$P$S$A$B$V$H$Y$C$V$I$F$V$R$I$Q$G$V$E$Y$T$P$A$C$H 192
Db 109 L$G$Y$I$Q$T$K$G$N$I$V$G$T$G$S$F$A$L$L$T$T$P$M$A$H$S$E$M$E$F$V$A$V$I$E$G$F$E$G$V$T$P$P$O$T$H$ 168
QY 193 I$N$K$A$P$P$L$E$R$S$R$L$T$T$A$F$C$S$Y$G$A$V$V$A$M$P$A$G$V$L$V$Q$S$M$S$V$F$P$V$V$S$F$G$I$P$W$T$P$W 252
Db 169 V$A$R$M$S$P$P$L$E$R$R$M$S$I$A$F$A$G$N$Y$A$C$T$V$A$M$C$S$G$F$L$T$K$Y$G$B$E$V$F$V$F$G$T$G$V$M$T$W 228
QY 253 L$V$Y$E$S$P$A$H$B$S$I$E$B$E$R$K$Y$I$E$D$A$I$G$S$A$K$M$P$L$T$K$F$T$P$W$R$F$F$T$S$M$P$V$A$I$V$A$N$F 312
Db 229 L$V$P$V$K$G$F$E$L$D$F$C$S$K$E$C$D$Y$I$Q$T$G$Y$V$G$S$-----K$H$V$K$P$M$R$A$I$F$T$S$M$P$A$I$M$A$S$H$P 283
QY 313 C$R$W$T$Y$T$Y$L$L$I$Q$D$P$Y$F$E$E$V$G$F$E$S$K$G$V$S$A$L$P$H$L$W$T$T$Y$V$I$G$Q$A$L$D$P$A$R$S$R$I$M$S 372
Db 284 S$E$M$W$G$Y$T$L$T$Q$L$P$F$P$L$D$T$L$N$F$D$J$G$K$G$L$S$A$V$P$Y$A$M$G$L$L$A$V$S$Y$L$D$M$V$Q$V$G$I$W$T 343
QY 373 T$Y$N$V$R$L$A$N$C$G$F$G$E$A$T$L$L$V$G$S$H$S$K$G$V$A$I$F$E$V$L$A$V$G$S$G$F$A$I$G$F$N$V$H$L$D$A$P$ 432
Db 344 T$Y$O$V$R$N$F$O$C$A$F$L$Q$Y$V$P$M$M$L$Y$A$L$D$P$T$M$S$V$S$L$I$N$A$G$L$A$F$A$M$S$G$A$V$V$H$L$D$A$P$ 403
QY 433 V$A$S$I$M$G$I$N$G$V$L$S$G$M$V$C$P$I$Y$G$A$M$T$K$H$T$R$E$M$Q$V$P$L$A$S$V$H$Y$G$V$T$Y$G$V$P$A$G 492
Db 404 H$A$S$V$L$M$G$I$N$T$F$A$T$P$G$I$V$S$P$L$T$G$V$V$T$N$O$T$S$E$M$R$I$F$F$I$S$A$G$I$V$W$C$V$T$Y$M$F$Y$C$G 463
QY 493 E$K$O$P$A$E$-P$E$M$S$E$-----K$G$P$G$H$Q$A$G$S$D$S$E$M$D 526
Db 464 D$L$O$E$M$A$K$T$P$E$Q$A$E$R$K$A$Q$O$L$T$O$T$A$G$V$-----N$G$A$E$K$D 502

```

```

RESULT 3
US-11-097-143-24411
Sequence 24411, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIORITY APPLICATION NUMBER: 60/157,832
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: 60/160,191
PRIORITY FILING DATE: 1999-10-19
PRIORITY APPLICATION NUMBER: 60/161,932
PRIORITY FILING DATE: 1999-10-28
PRIORITY APPLICATION NUMBER: 60/164,769
PRIORITY FILING DATE: 1999-11-12
PRIORITY APPLICATION NUMBER: 60/173,383
PRIORITY FILING DATE: 1999-12-28
PRIORITY APPLICATION NUMBER: 60/175,693
PRIORITY FILING DATE: 2000-01-12
PRIORITY APPLICATION NUMBER: 60/184,831
PRIORITY FILING DATE: 2000-02-24
PRIORITY APPLICATION NUMBER: 60/191,637
PRIORITY FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24411
LENGTH: 502
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-24411

```

Query Match	33.2%;	Score 986.5;	DB 7;	Length 502;
Best Local Similarity	38.0%;	Pred. No. 4.8e-71;		
Matches 200;	Conservative 96;	Mismatches 185;	Indels 45;	Gaps 7;

Qy 13 GRALCKRLHLEKROGAETLELSADGRPVTTQTRDPVVQCTCGELPRRYIAIMSGLG 72
 Db 10 GKHLEQVH-----ONNNEITE-----SEPLTFR-----FMRQRYIVLULAFG 48
 Qy 73 FCISGICNCGVAIVSVNNSTHRRGHVVVQKAFSMDPETVGLHGSFPMGYITQI 132
 Db 49 FPNVSLFVNLSVALVAMTEKRTVFDADGNVSQQDFPMDSKQKLLLSFFGYILTF 108
 Qy 133 PGFICOKFAANRVGFAIVATSTLMLIPSAARHYGCVIFVRLQGLVGVTPYACHG 192
 Db 109 LGGIYIGTIGGIVFGTIGSTAILTLTPMAASHLEMFLEFRILEGFFGVVPGIHA 168
 Qy 193 IWSKMAPLERSRLATTAFCCSYAGAVVAMPVLAVQYSGMSVFFYYGSGFLFMYLPM 252
 Db 169 VMARSPPLERSRNASIPAGNVACTVAVAMPCCSGLAKYGMESFFYFGTIGVNYITW 228
 Qy 253 LTVYESPALHPSISEERKTYIEDAIGESAKLMNLTFTSPWRFFTSMPYAIIVANF 312
 Db 229 LVFVYAGPELDRFCSKECDYIOKTIQYVGS-----KHVKHPWRAIFTSMPFYAIMASHF 283
 Qy 313 CRSMTEYLLISQPDYFEEVGFSEISKVGLVSALPHLMTIIVPIGQIADPLRSRIMS 372
 Db 284 SENNGFYLLTQLBSEFLDTNPFDLGKTGLISAVPYLAMGLLAVSGYLAOWLQYKGIWT 343
 Qy 373 TTNRYKLMNCCGFGMEATLLLVGYSHSGVAISFLVAVGFSFGAIGFNNHLDIAPR 432
 Db 344 TTYQRRNRCGAFIAGTYFMMLTAVLDPTWSVSLTAVGLGAPAWSGFAVNHLDIAPQ 403
 Qy 433 YASILMGISNGVTLGSCVPIIVGAMTKHKTREBQVYFLASIVHYGVIFPGVFPASG 492
 Db 404 HASVLMGIGTFATIPGISVPLTGVVVTQTSDEMRLIFLISAGIYLVGVCIYWFYCSG 463
 Qy 493 EKQPMAR-PEEMSER-----KCGFYGHQULASDSEMD 526
 Db 464 DLQEMAKTPEQKQAEERKQQLQTTAGFV-----NSGAEKLD 502

RESULT 4

US-60-655-875-146571
 ; Sequence 146571, Application US/60655875
 ; GENERAL INFORMATION:
 ; APPLICANT: Bouharov, Andrey
 ; APPLICANT: Du, Zifang
 ; APPLICANT: Guo, Zifang
 ; APPLICANT: Kovalic, David
 ; APPLICANT: Lu, Maolong
 ; APPLICANT: McCarter, James
 ; APPLICANT: Miller, Nancy
 ; APPLICANT: Williams, Deryck
 ; APPLICANT: Waudin, Mark
 ; TITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETERODERA INFESTATIONS
 ; TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
 ; FILE REFERENCE: 38-21(53885)
 ; CURRENT APPLICATION NUMBER: US/60/655,875
 ; CURRENT FILING DATE: 2005-02-24
 ; NUMBER OF SEQ ID NOS: 171306
 ; SEQ ID NO 146571
 ; LENGTH: 460
 ; TYPE: PRT
 ; ORGANISM: Heterodera glycines
 ; FEATURE:
 ; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID 72994; Strand=:; Position=1
 ; OTHER INFORMATION: -29,303-326,390-426,479-542,593-655,724-887,1213-1358,1574-1609,1
 ; OTHER INFORMATION: -1811,1864-1932,2321-2362,2432-2574,2676-2756,3152-3184,3631-3822
 ; FEATURE:
 ; OTHER INFORMATION: Homolog annotation: Hit ID=NF_499023.2; Match level="QueryCoverage
 ; OTHER INFORMATION: =99%; HitCoverage=72%; E-value=1e-144; Identity=59%; Hit descrip
 ; OTHER INFORMATION: EAting: abnormal pharyngeal pumping EAt-4; Nose Touch response
 ; OTHER INFORMATION: abnormal NOT-1; putative sodium-dependent
 ; US-60-655-875-146571

Query Match 31.2%; Score 927; DB 8; Length 460;

Best Local Similarity 45.6%; Pred. No. 2.6e-66;
 Matches 198; Conservative 51; Mismatches 113; Indels 72; Gaps 10;

Qy 172 VIFVRILOGLVGYTPYACG-----IWSKMAPLERSRLATTAF 211
 Db 10 VALVOIAGLVQGLAVPAMHGLVQGLAVPAMHGVCHMAVWCHMAVPLERSKLATTAF 69
 Qy 212 CG-----SYGAVVAMPVLAVQYSGM-----SSVFFYYGSGFLFMYLPLVS 256
 Db 70 TGSYAGAVFGLSYAGAVFGLPLSALVSYHMSMPFIYSMPFIYGVAGVIMSVFWSMT 129
 Qy 257 YESPALHPSISEERKTYIEDAIGESAKLMNLTFTSPWRFFTSMPYAIIVANFCSRW 316
 Db 130 FEKAFHFTIYQKQYIEADIG- PVOSSHPTVA-TIPWRALILSKPVAIIVANFASW 187
 Qy 317 TTYLLISQPDYFEEVGFSEISKVGLVSALPHLMTIIVPIGQIADPLRSRIMSTNV 376
 Db 188 NFYLLQVLTVMYMDVGLRISDSGLIAALPHAVMGCVLLIGRLADYLRNSKILSTAV 247
 Qy 377 RKLNNCCG-----FGMEATLLLVGYSHSGVAISFLVAVGFSFGAISG----- 421
 Db 248 RKLNNCCGFGCEALFLFVAYTSERTAMAFIHFIFSGFALSGFNNHLDIAP 307
 Qy 422 -----FVNHLDIAPRYASILMGISNGVTLGSCVPIIVGAMTKHKTREBQVYFLPIA 475
 Db 308 RYALIFVNNHLDIAPRYAAILMGFSNGIGTLAGTCTFVVSILTS-RNANGWTVFPIA 366
 Qy 476 SLVHYGVIFGYVPSGEGKQPMARPEEMSERKCGFVGHDLASDSEMDABEPGAP 535
 Db 367 SLHFTGTTFVAVASGELQWAEKPNNEE-----SSTDFFHQSTAOQNQNGTA 415
 Qy 536 APPP-SYGATHST 547
 Db 416 ATNPMPIGATTFT 429

RESULT 5

US-11-097-143-2895
 ; Sequence 2895, Application US/11097143
 ; GENERAL INFORMATION:
 ; APPLICANT: Venter, J. Craig
 ; APPLICANT: et al.
 ; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
 ; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
 ; FILE REFERENCE: CL000728
 ; CURRENT APPLICATION NUMBER: US/11/097,143
 ; CURRENT FILING DATE: 2005-04-04
 ; PRIOR APPLICATION NUMBER: 60/157,832
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: 60/160,191
 ; PRIOR FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 60/161,932
 ; PRIOR FILING DATE: 1999-10-28
 ; PRIOR APPLICATION NUMBER: 60/164,769
 ; PRIOR FILING DATE: 1999-11-12
 ; PRIOR APPLICATION NUMBER: 60/173,383
 ; PRIOR FILING DATE: 1999-12-28
 ; PRIOR APPLICATION NUMBER: 60/175,693
 ; PRIOR FILING DATE: 2000-01-12
 ; PRIOR APPLICATION NUMBER: 60/184,831
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: 60/191,637
 ; PRIOR FILING DATE: 2000-03-23
 ; NUMBER OF SEQ ID NOS: 43008
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2895
 ; LENGTH: 559
 ; TYPE: PRT
 ; ORGANISM: DROSOPHILA
 ; US-11-097-143-2895

Query Match 26.9%; Score 798; DB 7; Length 559;

Best Local Similarity 33.3%; Pred. No. 7.6e-56;
Matches 161; Conservative 97; Mismatches 184; Indels 42; Gaps 7;

```

QY 58 GLPRRIIIMSGISFGICRNCNVAIVSMVN-----NSTT-----HR 98
Db 64 GKRTIRIFSGFMGLGAAVYAMKVNLSVIAVAVNTALPHSSSVITDTCTPLPAPHN 123
QY 99 GGHVVQK-AQFSWDETVGLIHGSFPMGYIVTQIPGCFICQFANRVFPAIVATSTL 157
Db 124 GSDPNQKGEFVMDATQGLVIGSFYGVLTQVPGMAELYGKKIYGVGLITAYF 183
QY 158 NMLISAAVHYGCVTFVRILOGVGVTPYPCGHGWSKAPPLERSRLATTAFCGSYAG 217
Db 184 TLITPLAAMDPLVLVRIILRIGMGEGVTPAMHAMLAHMIPLERNKFAAIVYAGSNIG 243
QY 218 AVANMPLAGLVQ---YSGMSSVFYVYSGFIFWYLFMWLVESFALHPSISEERKYI 274
Db 244 TVISWPLAGWGLSGLDFLGMPSPAFYIFGLGLIMFAMMYLVYDKPSDPRISESERETI 303
QY 275 EDAI-----GSATLAMPITKFTSPWRFFTSMEVVAIIVANFCRSWT 317
Db 304 EKSLOQRILINDIAEABEEDGDEVSILAPPEEPIPMSSSLTSVPLMILITQCGQMA 363
QY 318 FVLILISQDPYEEVFGPEISKYGVSALPHLWMTIIVPIGQIADFLSRKIMSTTVR 377
Db 364 FYTQLEPFTYMSNIHFDIOSNALINAVPYLTSWFGIACSALDPMMLARRYSILANSY 423
QY 378 KLMNCGFCFMEATLLIVGYSKGVASIFVLAVG-FSGFALISGPNVNHDIAPRYASI 436
Db 424 KLMNVYASVPSIGLIGIIVGCDWVWVFMLANGVSGFAGVAYAGQMNHILSPRYAT 483
QY 437 LMGISNGVTLGSMVCPITVGAMTKHK-TREMOYVFLIASLVHYGVIFGVFASGEKO 495
Db 484 MGIINSAANIGCFIAPYIIGLINHRETLQWHLVFWLAAGLINAGNTIYLIFASAEQ 543
QY 496 PWAE 499
Db 544 SMSK 547

RESULT 6
US-11-097-143-27831
; Sequence 27831, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27831
; LENGTH: 516
; TYPE: PRT

```

ORGANISM: DROSOPHILA
US-11-097-143-27831

Query Match 25.9%; Score 769.5; DB 7; Length 516;
Best Local Similarity 33.7%; Pred. No. 1.3e-53;
Matches 165; Conservative 97; Mismatches 192; Indels 35; Gaps 10;

```

QY 43 TTQTPDPVVDCTCGLPRIYIAMSGLFCISFGICRNCNVAIVSMVNSTHRC--- 99
Db 12 TEKDEKPALGC---PATRYVTFMFLGMANNAVMTNMSVALVAVMNHTRAIISGEAE 67
QY 100 -----GHVV-----QRAQSWDETVGLIHGSFPMGYIVTQIPGCFICQFANRVG 148
Db 68 EYDDECGRDPIDIDSGEFAFMSALOGYILISFFGVIVTQIPFGILAKYGSILRFLG 127
QY 149 FAIVATSTLNMIPSAAR---VHYGCVTFVRILOGVGVTPYPCGHGWSKAPPLERS 205
Db 128 YAMLINVSFAFVPAARAGGVWGLCA--VRIQGLSGRPIVPCTHAMLAHMIPLERNSR 185
QY 206 LATTAFCSYAGAVVAMPPLAGLVQ---SGMSSVFYVYSGFIFWYLFMWLVESFAL 262
Db 186 MGAAYYAGAQFCTIISMPISGLLAEYFGDGMPSIFVYFGIVGTWSIAFLIFVHEDPS 245
QY 263 HPSISEERKTYEDAIAGESAKLAMPITKFTSPWRFFTSMPYAIIVANFCRSWTFYLL 322
Db 246 HPTIDEREREKTYINDSLMGTDVVKSP---PIPFKAIILSLPFYALIFAHMGHNYGETLM 301
QY 323 ISQDPYEEVFGPEISKYGVSALPHLWMTIIVPIGQIADFLSRKIMSTTVRKLAM- 381
Db 302 TELPFTYMKQVLFSLKSNGLSLDPLVLMMLSMITSVADMMISSKPSHTATKRLNS 361
QY 382 CGFGFMEATLLIVGYSKGVASIFVLAVGSGFALISGPNVNHDIAPRYASILMGIS 441
Db 369 IGQYRGVALIASYATGCRALTLITIGVLANGIYSGFIRNHLDTLPRAGFLMSIT 421
QY 442 NGVTLGSMVCPITVGAMTKHRE--EMOYVFLIASLVHYGVIFGVFASGEKOPWA 498
Db 422 NCSANILAGLIAPIAAGHILSDPSKPMQGMQIVFPIAAFVYIICGTFYNIIFSGSROYWD 481
QY 499 EPEEMSEK 507
Db 482 NPED-DEOK 489

RESULT 7
US-11-097-143-17844
; Sequence 17844, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008

```

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17844
LENGTH: 529
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-17844

Query Match 25.8%; Score 767.5; DB 7; Length 529;
Best Local Similarity 34.5%; Pred. No. 2e-53;
Matches 164; Conservative 94; Mismatches 185; Indels 33; Gaps 10;

QY 56 CEGLPRIYIAIMSGLFCISFGICNIGVAIVSNVNNSTHKG-----GHVV-- 104
DB 36 CFA--TRFYTFMELFGMANAYVNRKTNMSVAIVANVHTAIKSGABEYDECGDRDPI 93
QY 105 ---OKAQSNDPEVYGLIHGSPFWGYITQIPGCGTCKPFAANRYFGAIVATSLNML 161
DB 94 DSDQGEFAMSSALOGYLLSFFGYVITQIPFGILACKYSLRFLGYMLINSVFAFLV 153
QY 162 PSAAR---VHYGCVIFVRILQGLVEGVTPACHGWSKAPPLERSRLATTAFGSGYAGA 218
DB 154 PVAARGGVWGLCA--VAFIOGLGEGPIVCTHMLAKMIPPNERSKGAIVYAGQRF 211
QY 219 VVAMPAGVLVQY---SGMSSVFYVYSGFGIFWYLFMLVSESPALHPSISEBERKYTE 275
DB 212 IISMPISGLAEYGDGCMPSIFVYFGIVGTWMSAFLFVHEDSSHPITIDEREKKYIN 271
QY 276 DAIESAKMLNPTRKSTPWRPFTSMFVAIIYANFCRSWTFYLLISQDYEEVYGF 335
DB 272 DSLGTGVVKS---PIPFYAIKSLPFYAILFAMHMGNYGELMTLEPTVMKQVLR 327
QY 336 EISVYGLVASALPHLWMTIIVPIGGQIADPLSRBRIMSTNTRKLMN--CGSGMEATLLV 394
DB 328 SLKSNGLSSLPYLAAMLPSMFISVADWMLSSKPSHTATRKLNISGQYGPVALTAA 387
QY 395 VGYSHSKGVAISFLVAVGSGFAISGFNVNHLDIAPRYASILMGISNGVTLGMCVPI 454
DB 388 SYTCDBALTLAILTIGVANGIYSGFKINHDLTPRFAGFMSITNSANLWGLAPI 447
QY 455 IVGAMTHKTR---EMQYVFLASLVHYGCVIFVGFVASEGKOPMAPEEMSEK 507
DB 448 AAGHLISDPKPMQWQIVFFIAFVYIICGTFYNIFGSGERQWDPED--DEQK 502

RESULT 8
US-11-097-143-5532
Sequence 5532, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CLO000728
CURRENT APPLICATION NUMBER: US/11/097,143
PRIOR FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5532
LENGTH: 493
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-5532

Query Match 25.2%; Score 747; DB 7; Length 493;
Best Local Similarity 33.3%; Pred. No. 8.1e-52;
Matches 158; Conservative 93; Mismatches 187; Indels 36; Gaps 8;

QY 58 GLPR-----RYIIAMSGLFCISFGICNIGVAIVSNVNNSTHKG----- 92
DB 8 GLQVRNPLSCROYLNLITMLGFLNVALRNLITAIIVDRPVNTSAVNATLVGNSTAA 67
QY 93 NSTTHRGHVYVQAQSGNDPEVYGLIHGSPFWGYITQIPGCGTCKPFAANRYFGAIV 152
DB 68 NSTASPDG--VDVYEREPWDSYQTNFVYLCGFPWGYITTELPGRLABELIGRRVFGHSM 126
QY 153 ATSLTNMLIPSAARVHYGCVIFVRILQGLVEGVTPACHGWSKAPPLERSRLATTAF 212
DB 127 WASLTLITPLAAHINVTVLIVRVVGLGASWPAIHVPAAVMIPPNERSKGAIVYAG 186
QY 213 GSYAGAVVAMPAGVLVQYSGMSSVFYVYSGFGIFWYLFMLVSESPALHPSISEBERK 272
DB 187 SS--LGAALTPWICGYLLSVAGMASVFLVTGAVGLMSLAWTFYETPHTPRIABERR 245
QY 273 YIEDAIESAKMLNPTRKSTPWRPFTSMFVAIIYANFCRSWTFYLLISQDYEEV 332
DB 246 EIEBAIGTTTSKRP---SHVPMQQLCSPAVMAIIICHLAVGFFVTVNQLPTFMSKI 302
QY 333 FGEISVYGLVASALPHLWMTIIVPIGGQIADPLSRBRIMSTNTRKLMNCGFGMEATLL 392
DB 303 LHPDIKONGLPSSLPYIGKYVMAVASSYLDYLLKKGTSTTATRKLTFTTALVYPCILM 362
QY 393 LV---VGYSHSKGVAISFLVAVGSGFAISGFNVNHLDIAPRYASILMGISNGVTLG 449
DB 363 IVQYFLGYDWTASTI--FSLALFAHGAIVTAGVNGDIAPNCGTIFGLANTLSRSG 420
QY 450 MWCPDIIVGAMT--KHKTREBQYVFLASLVHYGCVIFVGFVASEGKOPMAPEE 502
DB 421 FLTSMVQALTYKQOSFHSWQIVFWIILATYISAADVAILGSGELPWNPNPE 474

RESULT 9
US-60-669-241-29729
Sequence 29729, Application US/60669241
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Baum, James A
APPLICANT: Gilbertson, Larry A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLA
FILE REFERENCE: 38-21(53596)
CURRENT APPLICATION NUMBER: US/60/669,241
PRIOR FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60560842
PRIOR FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60565632
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60579062
PRIOR FILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: 60603421
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60617261
PRIOR FILING DATE: 2004-10-11
NUMBER OF SEQ ID NOS: 50011

```

; SEQ ID NO 29729
; LENGTH: 477
; TYPE: prt
; ORGANISM: Lygus hesperus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; OTHER INFORMATION: Coding regions on vcdna: vcdna=SeqID_4813; Strand=+; Position=6-1
; FEATURE:
; OTHER INFORMATION: Homolog annotation: Hit ID=XP_317786.1; Match Level=QueryCoverage
; OTHER INFORMATION: =89%, HitCoverage=92%, E-value=1e-134, Identity=50%; Hit descrip
; OTHER INFORMATION: ENSANGP000022197 [Anopheles gambiae]
; FEATURE:
; OTHER INFORMATION: Gene Ontology Annotation: Molecular function=inorganic phosphate
; OTHER INFORMATION: transporter activity; Cellular component=integral to membrane;
; OTHER INFORMATION: Biological process=phosphate transport
; FEATURE:
; OTHER INFORMATION: Pfam annotation: Pfam_ID=WFS_1; Match Level=Score=203.1, E-value
; OTHER INFORMATION: =5.6e-58, Copies=1; Pfam description=Major Facilitator Superfam
US-60-669-241-29729
```

```

Query Match      24.4%; Score 726; DB 8; Length 477;
Best Local Similarity 33.0%; Pred. No. 3.8e-50;
Matches 141; Conservative 88; Mismatches 178; Indels 20; Gaps 3;
```

```

QY 59 LPRRYIAIMSGLFCISFGICRNLGVAIVSMVNSTTRGGHVVVYQKA----- 107
DB 26 IQRVYLGIMGFLAVANATAMGILNLTENVVAPKNAHHVDDPNACPGILEVXKHT 85
QY 108 ---GFMSDPEITVGLIHGSFFWGYIVTQIPGCFICQKFAANRVGFAIVATSTLNLIPS 163
DB 86 DENNEFDMDEQIQGYILSAFYWGYYVTLHPGGLAQRFQKQTLGILGIVTLTLPF 145
QY 164 AARVHGCYIFRILOGLVGVTPYRACHGINSKAPLERSRLATTAFCGSAGAVVAMP 223
DB 146 AARAGPMLIAVRLLEGLGEGTTFPALNQLAQWPELRGRLGSIVFAGNIGTVSSA 205
QY 224 IAGVLVOYSGMSVVFYVYSGFGLFWYLFMLVLSYESPALHPSISEERKYIDAIAGESAK 283
DB 206 LSGLLLDVVDNPIILYIFRSAGVLMYVFIPLCYNDPASHPTTEREKYLETIGGIRK 265
QY 284 LNNPLTKFSTPWRPRTSMRYAIIIVANFCRSMTFYLLISQPDYFEEVGFEEISVGLV 343
DB 266 KEH---LKPWGSMASTSLPLMALITQIGHDMGLFTIOTDLPKWKSVTKRSIYONGIL 321
QY 344 SALPHLVMTIIVPIGQIADFLRSRIMSTTVRKLMMCGGEMETLLLVVYSHSKAV 403
DB 322 TSLPFLVMTAIGAGIIDLFLKKKWSVTGKRKVTFTIASVGPALGVILASVAGCDRV 381
QY 404 AISPL-VLAVGFSGFASIFGNVHLDIAPRYASILMGISNGVGLSGWCPIIVGAMTKH 462
DB 382 AATATFLVGMAMFGFYPYSLKYNALDLSINYAGTLMALVNGIGAIISGITPFLIXITPD 441
QY 463 KTRSEMQ 469
DB 442 QTMEMER 448
```

```

RESULT 10
US-11-097-143-11013
; Sequence 11013, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
```

```

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
```

```

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11013
; LENGTH: 496
; TYPE: prt
; ORGANISM: DROSOPHILA
US-11-097-143-11013
```

```

Query Match      24.2%; Score 719.5; DB 7; Length 496;
Best Local Similarity 32.6%; Pred. No. 1.3e-49;
Matches 163; Conservative 92; Mismatches 192; Indels 53; Gaps 12;
```

```

QY 57 FELPRYIAIMSGLFCISFGICRNLGVAIVSMV--NNST-----THR 98
DB 15 FVTPRVLIAIMGFLAIIAATYMRVCLQALITLVVYKNSITDDSEALCEPDIDEGTSV 74
QY 99 GGHVVVQKAPQSWDETVGLIHGSFFWGYIVTQIPGCFICQKFAANRVGFAIVATSTLN 158
DB 75 GG-----DFWSEBELQGLISLISFYIGYIVTHIPGGLAEKFGKWTLLGILSTAVFT 127
QY 159 MLIPSAKVHNG---CVFVRILOGLVGVTPYRACHGINSKAPLERSRLATTAFCGSY 215
DB 128 MLTPLA--INKKDSMDLITVRLMGLGEGTTFPALSVLLAAMVPANERGRKGLAVLGQQ 185
QY 216 AGAVAMPPLAGVLVOYSGMSVVFYVYSGFGLFWYLFMLVLSYESPALHPSISEERKYIE 275
DB 186 VGTIGNLISGVFIAYAGMEFVYFPGGLGVVWPAIIMFLCYSDTSHPIKPSREYIV 245
QY 276 DAIGESAKL--MNPPLTKFSTPWRPRTSMRYAIIIVANFCRSMTFYLLISQPDYFEEVF 333
DB 246 KEIGTISRNEDELPP-----TPWKALITNLPMPALVAAQIGHDMGFYIMVTDLPKYMADVL 300
QY 334 GEISKVLGVALPHLVMTIIVPIGQIADFLRSRIMSTTVRKLMMCGGEMETLLLV 393
DB 301 QPSIRANGLYSBLPYVMWIVSVSGFVADWIRRGVLTNTTRKVMT--GLAAFPAIF 358
QY 394 VVGYSHS---KGVASFLVLAVGFSGFASIFGNVHLDIAPRYASILMGISNGVGLSGM 450
DB 359 MVGASVYAGCDRVLVVYVLTICGLMGAYYAGKLSPLDMSFPACTLMAITIGIAITCV 418
QY 451 VCPITVGMATKHKTRSEMQVFLASLVHGYGVIFYGVAFSGEKPM---AEPE---E 502
DB 419 ITPYLAVMTTPASLSLEWLVFWVAFVGLCTFAVYICWASGEVQFPNNAPIQPSVDPE 478
QY 503 MSEKCGFVGHDLAAGSDS 522
DB 479 AQERK---VGEEKTSGLEBS 495
```

```

RESULT 11
US-11-097-143-20922
```

```

; Sequence 20922, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: DROSOPHILA GENES.
```



```
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO: 20922
LENGTH: 465
TYPE: PRT
ORGANISM: DROSOPHILA
US-11-097-143-20922

Query Match      24.1%; Score 716.5; DB 7; Length 465;
Best Local Similarity 31.8%; Pred. No. 2.1e-49;
Matches 143; Conservative 107; Mismatches 189; Indels 11; Gaps 6;

QY 56 CFCGLPRRYIIAMSGFRCISGRCNIGVAIVSNVNNSTTRGHVVV---QKAGQSW 111
DB 6 CFYVYKRNIALIMLMACILSTMMRVNLSINITIAWEDTSSHENGTEVEALPDYGPRTNW 65
QY 112 DPEVGLHGFSEFWGYVTOIPGCFICQFAANRVGFPAIVATSTLMLIPSAARVHYGC 171
DB 66 TQSDQALLGAVFYGYMTSLPAGTLAEMLGARNVAGSCLVAGLTLTLPAAAMDKXA 125
QY 172 VIFPAILOGVEGVTPYPCHGIMSKWAPPLERSRLATTAFCGSYGVAVVAMPPLAGVLVOY 231
DB 126 VFAVAFLLGLFNGVVPYPCCHSLVSKSPDEKGFVASIMGGTF-GTVIWPISGVIIEN 184
QY 232 SGMSVFVYVSGFGLFWLFWMLVSESPALHPSISEERKXTIEAIDESAAMLPDKF 291
DB 185 LGMDMAFIVIGLFWLVVAIMFYVADTPAOSTISLKERETESSLDOT--LSN-KKK 240
QY 292 STPMRFPTSMFVVAIIIVANFCRSWTFYLLISQPDYEEVGFESKGLVSAALPHLM 351
DB 241 WPRYKELVLSLPFWSLMLHVSMMGLFPLIATPKFLSEVGLFNLSSAGFLSLPHYAR 300
QY 352 TIIVPIGQIADFLRSRIMSTTVNRKLMNCGGFEMEATLLVGVY-SHSGKVALISPLVL 410
DB 301 LLCAFGFAVADVIMRRGMLSTVRMRKAFCLPESHILPGWMLITLAVFGDRDPVCAIMTI 360
QY 411 AVGESGFALISGRNVNHLIAPRYAIIIMGISNGVTLTSGMCPITIVGAMTKK-TREEMQ 469
DB 361 SLGFGAATVSNLNASQDLAPYACTLGIINCVCVTGPGISPLIIVAAFTKMENTIDDMH 420
QY 470 YVFLIASLVHYGVIFYGVFASGEKQPMAS 499
DB 421 WVFIIIGAAAYIILPALFFWVFGSKIKQKNE 450

RESULT 12
US-60-669-175-21828
Sequence 21828, Application US/60669175
GENERAL INFORMATION:
APPLICANT: Monsanto Technology LLC
APPLICANT: Baum, James A
APPLICANT: Gilbertson, Larry A
APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
```

```
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROL OF INSECT INFESTATION IN PLP
FILE REFERENCE: 38-21(53597)
CURRENT APPLICATION NUMBER: US/60/669,175
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60560842
PRIOR FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: 60565632
PRIOR FILING DATE: 2004-04-27
PRIOR APPLICATION NUMBER: 60579062
PRIOR FILING DATE: 2004-06-11
PRIOR APPLICATION NUMBER: 60603421
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60617261
PRIOR FILING DATE: 2004-10-11
NUMBER OF SEQ ID NOS: 40774
SEQ ID NO: 21828
LENGTH: 465
TYPE: PRT
ORGANISM: Diabrotica virgifera
FEATURE:
NAME/KEY: misc feature
LOCATION: (147)..(148)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (166)..(166)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (181)..(181)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (172)..(172)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (181)..(181)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
OTHER INFORMATION: Coding regions on vcdna: vcdna=seqID_1525; Strand=+; Position=189
OTHER INFORMATION: Homolog annotation: Hit ID=EXLJ1894.1; Match level=QueryCoverage
OTHER INFORMATION: =92%, HitCoverage=89%, E-value=1e-160, Identity=63%; Hit descrip
OTHER INFORMATION: GA18114-PA [Drosophila pseudobscura]
FEATURE:
OTHER INFORMATION: Gene Ontology Annotation: Molecular function=inorganic phosphate
OTHER INFORMATION: transporter activity; Cellular component=integral to membrane;
OTHER INFORMATION: Biological process=phosphate transport
FEATURE:
OTHER INFORMATION: Pfam annotation: Pfam ID=MFS_1; Match level="Score=180.8, E-value
OTHER INFORMATION: =2.9e-51, Copies=1"; Pfam description=Major Facilitator Superfam
US-60-669-175-21828

Query Match      23.8%; Score 708; DB 8; Length 465;
Best Local Similarity 33.4%; Pred. No. 1e-48;
Matches 155; Conservative 91; Mismatches 176; Indels 42; Gaps 11;

QY 24 EKROGAATLLESDGRVTTQTRDPVDCQ-CFGLPRRYIIAMSGFRCISGRCN 82
DB 9 ESNGBESTSEVED-EDETTRILIPVEVEDTINC--MKARITLILGLGFAANYAMKN 65
QY 83 LGVAIVSMVN-----NSTHKGHVYVQKQFSMDPEFVGLHGSFF 124
DB 66 LSAIVAVNVNTQPVFTNNSYDHCPIITDNTNG---TATPGSEFMDDEKQSIYLSGFF 122
QY 125 WGIYVTOIPGFIQCKPAANRVGFPAIVATSTLMLIPSAARVHYGCYIFRIIQL-V 183
DB 123 YGYVLTQVPGRIAEIGSKRVYGXVLTISFTLLTPPIARKMLHYLXRVVLEGKXE 182
QY 184 GVTYPACGIMSKAPPLERSRLATTAFCGSYGVAVVAMPPLAGVLVOY---SGMSVFVYV 240
```

Db 183 GUTPSSMAMLMARIPPLERSKFAAYVYAGTNGTLLSLPISGWLCSLKLNDGWPISFYI 242

Qy 241 YGSFGIFWYLFMLVSYESPALHPSISEEERKXIYEDAGESAKMNPITKFTPMRRPFT 300

Db 243 FGVLGIWVLFVWLLYDTPMSPHRIIDPQEKAFILMSICP---QDDROTSSIPWKHMR 298

Qy 301 SNPVVAIIVANCRSMTFFLLLSIDPDYEEVFGFEISKVGLVSALPHLVMITIIYDIGO 360

Db 299 CPELWAILVTOCGQSWAFYTOLEPTVMAQILHFDIQSDALLSAVPFTSW---IGGI 354

Qy 364 I-----ADFLRSRINSTVNRKLMNCGFGMEATLLLVGYSHSKGVAISPLV-LAVGFS 415

Db 355 LRSIFDMLLSKGYLSLSTSYKVNVSASVIPSIGLGAIVGCDKVAQQLALATATG 414

Qy 416 GFALSGFVNHLDIAPRYASILMGISNGVTLSGWCPIIVGAM 459

Db 415 GAVYAGNQMNHIALSPQYAGTWYGINSAANCGFLAPYIGLL 458

RESULT 13

US-11-097-143-28257

/ Sequence 28257, Application US/11097143

/ GENERAL INFORMATION:

/ APPLICANT: Venter, J. Craig

/ APPLICANT: et al.

/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

/ TITLE OF INVENTION: DROSOPHILA GENES.

/ FILE REFERENCE: CL000728

/ CURRENT APPLICATION NUMBER: US/11/097,143

/ CURRENT FILING DATE: 2005-04-04

/ PRIOR APPLICATION NUMBER: 60/157,832

/ PRIOR FILING DATE: 1999-10-05

/ PRIOR APPLICATION NUMBER: 60/160,191

/ PRIOR FILING DATE: 1999-10-19

/ PRIOR APPLICATION NUMBER: 60/161,932

/ PRIOR FILING DATE: 1999-10-28

/ PRIOR APPLICATION NUMBER: 60/164,769

/ PRIOR FILING DATE: 1999-11-12

/ PRIOR APPLICATION NUMBER: 60/173,383

/ PRIOR FILING DATE: 1999-12-28

/ PRIOR APPLICATION NUMBER: 60/175,693

/ PRIOR FILING DATE: 2000-01-12

/ PRIOR APPLICATION NUMBER: 60/184,831

/ PRIOR FILING DATE: 2000-02-24

/ PRIOR APPLICATION NUMBER: 60/191,637

/ PRIOR FILING DATE: 2000-03-23

/ NUMBER OF SEQ ID NOS: 43008

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 28257

/ LENGTH: 475

/ TYPE: PRF

/ ORGANISM: DROSOPHILA

US-11-097-143-28257

Query Match 23.6%; Score 699.5; DB 7; Length 475;
Best Local Similarity 33.1%; Pred. No. 5.1e-48;
Matches 149; Conservative 91; Mismatches 197; Indels 13; Gaps 6;

Db 190 SIFYSIGGICGWSVYVFFFGAGSPQECKSISAEKULIENSQADEVSGGQEPKEQLPT 249

Qy 294 PMRRPFTSNPVYAIIVANFCRSMTFFLLLSIDPDYEEVFGFEISKVGLVSALPHLVMIT 353

Db 250 PHLSPFTSPAPLVLLVLSVHNHGWFTLLTEIPSYMKNLIGDKISNALLSLPYWCMPA 309

Qy 354 IYPIGGQIADFLRSRINSTVNRKLMNCGGMEATLLLVGYSH--SKGVAISFLVLA 411

Db 310 MSFVSSISAQUNNCRISRSRLFNISGIMIPWTVLVGIVNPDQSELAVVLLCFT 369

Qy 412 VEPSEFALSGFVNHLDIAPRYASILMGISNGVTLSGWCPIIVG-AMTKHKTSEMOY 470

Db 370 VMMNGATYIGFTNHIIDSPNPAIGILMGITNGVANIMSIAPLVGFIYTNHDEBQMRI 429

Qy 471 VFLIASLVHYGVIFEVGFASGEKQPMAP 500

Db 430 VFFLIAGFLVGNLTLYVIFGKANYQPMNDP 459

RESULT 14

US-11-097-143-37224

/ Sequence 37224, Application US/11097143

/ GENERAL INFORMATION:

/ APPLICANT: Venter, J. Craig

/ APPLICANT: et al.

/ TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

/ TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

/ TITLE OF INVENTION: DROSOPHILA GENES.

/ FILE REFERENCE: CL000728

/ CURRENT APPLICATION NUMBER: US/11/097,143

/ CURRENT FILING DATE: 2005-04-04

/ PRIOR APPLICATION NUMBER: 60/157,832

/ PRIOR FILING DATE: 1999-10-05

/ PRIOR APPLICATION NUMBER: 60/160,191

/ PRIOR FILING DATE: 1999-10-19

/ PRIOR APPLICATION NUMBER: 60/161,932

/ PRIOR FILING DATE: 1999-10-28

/ PRIOR APPLICATION NUMBER: 60/164,769

/ PRIOR FILING DATE: 1999-11-12

/ PRIOR APPLICATION NUMBER: 60/173,383

/ PRIOR FILING DATE: 1999-12-28

/ PRIOR APPLICATION NUMBER: 60/175,693

/ PRIOR FILING DATE: 2000-01-12

/ PRIOR APPLICATION NUMBER: 60/184,831

/ PRIOR FILING DATE: 2000-02-24

/ PRIOR APPLICATION NUMBER: 60/191,637

/ PRIOR FILING DATE: 2000-03-23

/ NUMBER OF SEQ ID NOS: 43008

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 37224

/ LENGTH: 491

/ TYPE: PRF

/ ORGANISM: DROSOPHILA

US-11-097-143-37224

Query Match 23.6%; Score 699.5; DB 7; Length 491;
Best Local Similarity 33.1%; Pred. No. 5.3e-48;
Matches 149; Conservative 91; Mismatches 197; Indels 13; Gaps 6;

Qy 58 GLPRRYIIMSGLGFICFSGIRCNLGVAIYSMNNSSTTHRGHVVYQKAGSSMPDEYTG 117

Db 16 GGVHGFVOLLFFALTVAVYGCVRNLSVAVVAMTDAAS-----VNPDPPEYVMSKTKS 69

Qy 118 LHHGFFMGYITQIPGGFICQKFAANRVFGFAIVATSTLMILPSAARV-HYGCVIIVR 176

Db 70 LLLSFFMGYITQVPAGQIARKYGGKWMILSGLAICSTLINTLPICAKIGQMOLVCAIR 129

Qy 177 ILQGLVEGVTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYS-GWS 235

Db 130 VVEGICQGVFPSTHTTILSQWAPPKERATLTGCAVSGNQFGTILMLATSGVIAASPIGMP 189

Qy 236 SVFYVYGSFGIFWYLFMLVSYESPALHPSISEEERKXIYEDAGESAKMNPITKFTST 293

Qy 58 GLPRRYIIMSGLGFICFSGIRCNLGVAIYSMNNSSTTHRGHVVYQKAGSSMPDEYTG 117

Db 32 GGVHGFVOLLFFALTVAVYGCVRNLSVAVVAMTDAAS-----VNPDPPEYVMSKTKS 85

Qy 118 LHHGFFMGYITQIPGGFICQKFAANRVFGFAIVATSTLMILPSAARV-HYGCVIIVR 176

Db 86 LLLSFFMGYITQVPAGQIARKYGGKWMILSGLAICSTLINTLPICAKIGQMOLVCAIR 145

Qy 177 ILQGLVEGVTPACHGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVOYS-GWS 235

Db 146 VVEGICQGVFPSTHTTILSQWAPPKERATLTGCAVSGNQFGTILMLATSGVIAASPIGMP 205

Qy 236 SVFYVYGSFGIFWYLFMLVSYESPALHPSISEEERKXIYEDAGESAKMNPITKFTST 293

Db 206 SIFYISGGIGCVMSVYFFPFPGAGSPQCKSISAEBKKLTJEMSGADBSGGQEQPKQLPT 265
 Qy 224 PWRFFTSMPVYAIIVANCRCSWTFLLLISQDPDVEEYFGFEISKGLVSLAPHLVMTI 353
 Db 266 PMLSEFTSPAPLVLLVSHSNVNMWGFMTLLTEIPSYMKNTLIGDKIKSNALLISLPPYCMFA 325
 Qy 354 IVPIGGOIADPLRSRIMSTTVNRKLMNCGCFMEATELLLVVGYSH-SKGVASIFVLA 411
 Db 326 MSFVSSLSIAQNNNNNCISRSRSTRKLFNSIGLIMPVTLVGLGYVNPDSGEALVLLCFT 385
 Qy 412 VQFSGFASIGENVNHLDIAPRYASIIIMGISNGVLTSGWCPPIIV-AMTKHTRREMOY 470
 Db 386 VGMNATVLTGFNTNHIIDLSPNFAGILMGITNGVANIISIIAPLVIGFVITNEHDPEQWRI 445
 Qy 471 VELLASLVHYGVIFRYGVASEKQPMABP 500
 Db 446 VFETIAGFYLVGNLTLYIFGRKANVQPMNP 475

```

RESULT 15
US-11-097-143-9567
; Sequence 9567, Application US/11097143
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9567
; LENGTH: 512
; TYPE: PRT
; ORGANISM: DROSOPHILA
; US-11-097-143-9567

```

Query Match	30.5%	Score 698.5	DB 7	Length 512
Best Local Similarity	30.7%	Pred. 6.7e-48		
Matches	160	Conservative 103	Mismatches 192	Indels 67
			Gaps	12
QY	59	LPRRYITAIIMSGLEFCISFSGIRCNLGVAIYSMNST--TH-----RCGH-----	101	
Db	16	VPARIVTLLIGSISGMALVYGLKVLMSVMVMNHTAKHGDGGGHHGSVILSNASQ	75	
QY	102	-----VVYQKAQFSMDPEYVLGHSGFPMGYIYTOIPGFTICQFPAAN	144	
Db	76	VSLVEBCNPGCAGSNVTAKVDGCPFDMSBPQGTLLSCYFNGYLSQIPLHAVENFSAK	135	
QY	145	RVFGFAIVATSTLMLIPSAARVHYGCIYFRIIOGLEGTGYTPACHGIGSKWAPLEBS	204	
Db	136	WYMFVSAIVNYCVLLTPVTEIHHGGLIKRVLIEGVGGSGSFLPMHMYISKAPPTBRM	195	
QY	205	RLATTACGSAAGAVVAMPPLAGVLVQYSGMSGFYVYGSFGIFWTLFWLLVSYSPALHP	264	

Db 190 VMSIIIVGTSAGTALSTLILLAGVSAQKQWESVFPVWGALSCIMMLLVLLVYQDNPKQR 255

Qy 265 SISEERKTIEDALIGESACL-MNPITKSTPWRKRPFTSMRYATIVANFCRSMTFFYLLI 323

Dp 256 FISLERQMTSSSLGTEQKTEHHP---AVWKGKFTSVSPFWALLIHTQSNFQWYMFLLI 311

Qy 324 SQDYEEYEFGEISKVQVLSALPLVNTIIIVPIGQIADFLRSRRIMSTTNVAKLMAN-- 384

Dp 312 RIFPYMKQYLKFNVASNNALSLALPYFPWIIIFSICGLKLDLQKKGITTTVAARKTATSI 371

Qy 382 CGGF-GMEATLLLVYSHSKVALSLFLVLAVG--SGFALSGNNVHLLIAPRYASILM 438

Dp 372 CTLLIPVCLLVICYIGCRHYEAVS---VMSVGVVANGSMSPGSLSHNHDIAPEPAGTIV 427

Qy 439 GISNGVGLTSGWVCPDIVGAMTK-HKTREEKQYVFLASLVHYGCVFYGVFASGEKQPM 497

Dp 428 ALTNLTATLTPIGLVPLFVGFTKGNQNGIARIIIFGTIVLFALEPLVFLVLSGSPQM 487

Qy 498 AEPEEMSEKQGVFHDQLAGS-DSEMEDDAEPPGAPRAPR 538

Dp 488 NK-----AGTPKDPKEMKDEKTPKELTPK 512

Search completed: June 2, 2005, 11:42:03
Job time : 58 secs

Job time : 58 secs

... PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:20:37 ; Search time 42 Seconds
(without alignments)
1282.890 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEPRQEEPRKLGRALGKLM.....YGATHSTFPQPPRPVVDY 560

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2925	98.5	560	2 159302	brain specific Na+ protein ZK512.6 [i
2	1297	43.7	576	2 H88548	probable sodium-de
3	1294	43.6	563	2 T43650	hypothetical prote
4	971	32.7	573	2 T23589	hypothetical prote
5	950	32.0	544	2 T24633	hypothetical prote
6	885	29.8	466	2 S40767	hypothetical prote
7	775.5	26.1	493	2 G88553	protein C38C10.2 [
8	763.5	25.7	472	2 S28286	hypothetical prote
9	720.5	24.3	512	2 H84698	hypothetical prote
10	685.5	23.1	465	2 A56410	sodium/phosphate t
11	626.5	21.1	467	2 A48916	sodium phosphate t
12	619	20.8	465	2 S69915	sodium-phosphate t
13	616.5	20.8	465	2 T19473	Na+-dependent phos
14	596.5	20.1	433	2 T01534	hypothetical prote
15	471	15.9	537	2 T45634	hypothetical prote
16	466.5	15.7	501	2 D84800	hypothetical prote
17	455.5	15.3	561	2 B89135	protein P2566.7 [i
18	439.5	14.8	380	2 T29248	hypothetical prote
19	423.5	14.3	568	2 S44742	C02C2.4 protein -
20	422	14.2	592	2 T25419	hypothetical prote
21	403	13.6	516	2 T24729	hypothetical prote
22	396	13.3	445	2 T23590	hypothetical prote
23	394	13.3	530	2 T29418	hypothetical prote
24	387.5	13.0	452	2 A50861	probable glucarate
25	385.5	13.0	450	2 A65061	probable glucarate
26	385.5	13.0	450	2 C85930	probable transport
27	385.5	13.0	450	2 A91085	probable transport
28	373	12.6	506	2 T29968	hypothetical prote
29	371.5	12.5	499	2 T15201	hypothetical prote

30	363.5	12.2	425	2 A90055	hypothetical prote
31	361	12.2	485	2 T24115	hypothetical prote
32	356	12.0	455	2 H69752	probable glucarat
33	338	11.4	659	2 T33557	hypothetical prote
34	337	11.3	543	2 T32496	hypothetical prote
35	330.5	11.1	444	2 B85974	probable galactara
36	330.5	11.1	444	2 B91129	probable galactara
37	330.5	11.1	444	2 C65102	probable galactara
38	328.5	11.1	487	2 T23776	hypothetical prote
39	325.5	11.0	420	2 S44900	ZK652.10 protein -
40	322	10.8	473	2 T31717	hypothetical prote
41	319.5	10.8	443	2 F89426	protein M162.5 [im
42	317	10.7	452	2 T33101	hypothetical prote
43	316	10.6	445	1 D65171	hypothetical 48.8
44	314	10.6	478	2 T33942	hypothetical prote
45	311.5	10.6	537	2 T20746	hypothetical prote

ALIGNMENTS

RESULT 1

159302
brain specific Na+-dependent inorganic phosphate cotransporter - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I59302
R:NI, B.; Rostek, P. R.; Nadi, N.S.; Paul, S. M.
Proc. Natl. Acad. Sci. U.S.A. 91, 5607-5611, 1994
A>Title: Cloning and expression of a cDNA encoding a brain-specific Na(+)-dependent inor
A:Reference number: I59302; MUID:94261635; PMID:8202535
A:Accession: I59302
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-560 <RES>
A:Cross-references: UNIPROT:Q62634; EMBL:U07609; NID:g507414; PIDN:AAA19646.1; PID:g5074

Query Match 98.5%; Score 2925; DB 2; Length 560;
Best Local Similarity 98.2%; Pred. No. 2.9e-229;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY	1	MEPRQEEPRKLGRALGKLMHRLERKROGARTLELSADGRPVTTQTRDPVVDCTCFGLP	60
DB	1	MEPRQEEPRKLGRALGKLMHRLERKROGARTLELSADGRPVTTHTRDPVVDCTCFGLP	60
QY	61	RRYIIAIMGSGFCISFGIRCNLGVAVISVNNSTTRHGGHVYQKQPSWDETVGLIH	120
DB	61	RRYIIAIMGSGFCISFGIRCNLGVAVISVNNSTTRHGGHVYQKQPSWDETVGLIH	120
QY	121	GSFPMGYIVTQIPGFCIQKPAANRVGFAIVASTLMMLIPSAARVHYGCVIVRIIQG	180
DB	121	GSFPMGYIVTQIPGFCIQKPAANRVGFAIVASTLMMLIPSAARVHYGCVIVRIIQG	180
QY	181	LVEGVTPACGIGSKAPLERSRLATFACGAYAGVAVMPAGVVOYSGMSSVFYV	240
DB	181	LVEGVTPACGIGSKAPLERSRLATFACGAYAGVAVMPAGVVOYSGMSSVFYV	240
QY	241	YGSFGIFWYLFMWLVSYESPALHPSISEEKKYEDAIIGESAKLMPLTKSTPMRRPFT	300
DB	241	YGSFGIFWYLFMWLVSYESPALHPSISEEKKYEDAIIGESAKLMPLTKSTPMRRPFT	300
QY	301	SMYPVAIIIVANFCRSWTFYLLIQPQDYFEVFGPEISKGLVSNALPHLVNTIIVPIQGG	360
DB	301	SMYPVAIIIVANFCRSWTFYLLIQPQDYFEVFGPEISKGLVSNALPHLVNTIIVPIQGG	360
QY	361	IADFLRSRIMSTNNVKKMCGFGMEATLLVVGSHSGVAISFLVLAVGSFGPAIS	420
DB	361	IADFLRSRIMSTNNVKKMCGFGMEATLLVVGSHSGVAISFLVLAVGSFGPAIS	420
QY	421	GFNNVHLDIAPRYASIIIMGISNGVGLTSGWVCPPIIVGAMTKGKRENOVYFLIASLVHY	480
DB	421	GFNNVHLDIAPRYASIIIMGISNGVGLTSGWVCPPIIVGAMTKGKRENOVYFLIASLVHY	480

QY	481	GGVIFGVGFASGCKQWAPREEMSEKCGFVGHDLAASDSEMEDELRPGADPAPP	540
		:	
Dd	481	GGVIFGVGFASGCKQWAPREEMSEKCGFVGHDLAASDSEMEDEVLPAGADPAPP	540
		:	
QY	541	YGATHSTFOPPRRPRPVRY	560
		:	
Dd	541	YGATHSTFOPPRRPRPVRY	560

RESULT 2

protein ZK512.6[imported] - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C/Accession: H88548
R/Anonymous: The C. elegans Sequencing Consortium.
R/Accession: 2001-2010-2000

A:/Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A:/Reference number: A75000; MUID:99069613; PMID:9851916
A:/Note: see websites genome.mucl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:/Accession: H68548
A:/Status: Preliminary
A:/Molecule type: DNA
A:/Residues: 1-576 <STO>
A:/Cross-references: UNIPROT:P34644; GB:chr_III; PIDD:CAA80150.1; PID:g3881690; GSPDB:GNM
C:/Genetics:
A:/Gene: ZK512.6
A:/Map position: 3

Query Match	43.7%;	Score 1297;	DB 2;	Length 576;
Best Local Similarity	47.7%;	Pred. No. 3.4e-97;		
Matches 262;	Conservative 88;	Mismatches 171;	Indels 28;	Gaps 10;

```

QY 9 RKAAGRALGKHRLHLEKKOEAGETLEISADSRPVTQTRDP---PVUDCTCFGJPR-RYI 64
Db 12 KQWVGEPLAKTAAATAAASATGAAPQOMGEENENPMQMSHKVLQVMEQTIIGCKRKMVL 71
QY 65 IAINSGAGFCISFGICRNLGVAVIVSNVNNSTTHRGHVYVQKQFSPMDPEVTGLHGSFF 124
Db 72 LAIIANNGFMISFGICRNFPGAATKTHMYKNYTDYPG--KVMEHFNMWITDELVSWESEYF 128
QY 125 WGYIVTQIPGFGFICQKPEANRVPFGAIVATSTLMNLPSAARVHYG-CVIFVRILQGLVE 183
Db 129 XGYIVTQIPAGFLAAKPPPNKLPFGGICGVAFNILLPYGKRVSDVIVATIQTLQGLVQ 188
QY 184 GVTTPACHGIGSKAAPLEERSRLATTAFCGSIAGAVVAMPPLAGVLVQYSGHSSVFTYGS 243
Db 189 GVCPPAHMGVWRVYAPAPMERSKLTATTAFTGSIAGAVILPLPSAFIVSVSMAAFYTLGV 248
QY 244 FGIWYLFMWLLVSVSPALHPSISEEKRVTIEDAIGESAKLMNPITKSTWRBPPFSTMP 303
Db 249 CGVIMAIMFECVTEKPRAPHPTISOEKLIFEDAIQHN-S-THPIR-SIPMKALVTSKP 306
QY 304 VYAIIVANECRSWTFYLLILISQPDYFEEVFGEFISKVGVLSPHLVNTIIVPIGQIAD 363
Db 307 VMAIIVANFASTWFYLLIQNLTYMKALKMKTADSGILAIIPHLVMGCVLVNGGQLAD 366
QY 364 FLRSERRIMSTNNVRKMMCGSGFGEATLLVGVSHSGVAILSPVLVAVGSGFASGFEN 423
Db 367 YLRSNKILSTIAVRKIFNCGGSGGEAPMLVVAITTSPTTAIMALIAVAGSGFASGFEN 426
QY 424 VNHLDIAPRVASIIIMGISNGVTLSGMVCPIIVGAMTGHKTRREMOVFLIASLVHYGV 483
Db 427 VNHLDIAPRVAAIIIMGFSNGIGTLAGLTCPPVTEAFTH-SKHGWTSVFLIASLIHFQV 485
QY 484 IFYGVAFSGEQPAAPEEMSE-----EKCGFVG-----HQULASDSEMEDE 527
Db 486 TFYVAVVYSGEIQEWAPREBEEMSENKELVNKTGINGTGVGAETTFYQLPAGVDSYSQAO 545

```

QY	528	AEP-PGAPP	535
Db	546	AAAPAGTNP	554

RESULT 3
T43650
probable sodium-dependent inorganic phosphate cotransporter - *Caenorhabditis elegans*

C:\Access

A;Description: EA1-4, a homolog of a mammalian sodium-dependent inorganic phosphate cotransporter
A;Reference number: Z22599

A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-563 <LE>
A:Cross-references: UNIPROT:Q9TN7, EMBL:AF095787, PIDD:AA064972.1
A:Experimental source: strain Bristol N2
A:Genetics:
A:Gene: eat-4
A:Map position: 3
C:Function:
A:Description: is necessary for glutamatergic neurotransmission

Query Match	43.6%;	Score 1294;	DB 2;	Length 563;
Best Local Similarity	47.9%;	Pred. No. 5.8e-97;		
Matches 262;	Conservative 86;	Mismatches 171;	Indels 28;	Gaps 10;

QY	11	L	A	G	A	L	G	T	H	L	L	E	K	R	O	G	A	T	L	L	S	A	D	R	V	T	T	O	T	R	P	---	P	V	D	C	C	F	G	I	R	-	R	Y	I	A	66										
Db	1	M	V	E	R	P	L	K	M	T	A	A	A	S	A	T	G	A	P	P	Q	M	O	B	E	G	N	E	N	P	Q	M	S	N	K	Y	L	Q	V	M	E	Q	I	W	I	C	K	R	M	I	L	A	60				
QY	67	I	M	S	G	L	G	C	I	S	F	G	I	R	C	N	G	V	A	I	V	S	V	N	N	S	T	T	R	G	H	V	V	O	K	A	F	S	M	D	E	T	V	G	I	H	S	F	P	W	6						
Db	61	I	L	A	N	G	F	M	I	S	F	G	I	R	C	N	F	E	G	A	K	T	H	Y	K	N	T	D	E	Y	G	---	K	V	H	M	E	F	N	W	T	I	D	E	L	S	M	E	S	S	E	Y	6				
QY	127	Y	I	V	I	O	I	R	O	G	F	I	C	O	R	E	A	N	R	V	G	F	A	I	V	A	T	S	T	L	M	L	I	P	S	A	R	H	Y	G	-	C	V	F	N	I	L	O	G	V	185						
Db	118	Y	L	V	I	O	I	P	A	G	F	I	A	A	K	F	P	P	N	K	L	F	G	F	G	V	G	A	F	I	N	T	L	P	Y	G	K	V	K	S	D	L	V	A	F	I	Q	T	O	G	V	177					
QY	186	T	Y	P	A	C	H	I	G	I	S	F	M	A	R	P	L	E	R	S	R	L	A	T	T	A	F	C	S	Y	A	G	A	V	A	V	A	M	P	L	A	C	L	V	O	Y	S	M	S	S	F	E	Y	Y	G	S	245
Db	178	C	Y	P	A	M	H	G	W	R	M	A	P	M	E	R	S	K	I	A	T	T	A	F	T	O	S	Y	A	G	A	V	I	D	E	L	S	A	F	L	V	I	S	Y	S	M	A	P	F	I	L	Y	G	V	237		
QY	246	I	F	W	L	F	M	L	V	S	E	S	P	A	L	H	P	S	I	S	E	E	R	K	I	E	D	A	I	G	E	S	A	K	L	M	P	L	T	K	S	T	P	M	R	R	F	T	S	M	P	Y	305				
Db	238	V	I	M	A	L	M	P	C	V	T	E	K	D	A	F	H	P	T	I	S	O	E	K	I	F	I	E	D	A	I	G	H	S	N	-	T	H	P	T	I	R	-	S	I	P	M	K	A	I	V	S	K	E	M	295	
QY	306	A	I	I	A	N	F	R	S	T	F	I	L	L	I	S	O	P	D	Y	E	E	V	E	V	G	E	I	S	K	G	L	V	S	A	P	H	L	M	T	I	I	P	G	G	I	A	D	F	L	365						
Db	296	A	I	I	A	N	F	R	S	T	F	I	L	L	I	O	N	Q	L	T	Y	K	E	A	L	G	M	K	I	A	O	S	G	L	I	A	A	P	H	L	M	G	C	V	I	M	G	G	L	A	D	Y	L	355			
QY	366	R	S	R	I	M	S	T	N	T	N	R	K	L	M	N	G	F	G	M	E	A	T	L	L	V	O	Y	S	H	S	K	G	V	A	I	F	L	V	A	E	F	S	G	A	I	S	G	F	N	425						
Db	356	R	S	N	K	I	L	T	T	A	R	K	I	F	N	C	G	F	G	E	A	F	M	L	I	A	Y	T	S	D	T	T	A	I	A	L	A	N	A	M	S	G	A	I	S	G	F	N	415								
QY	426	H	L	D	I	A	P	R	A	S	I	M	G	I	S	N	G	V	T	L	S	G	V	C	P	I																															

RESULT 4

hypothetical protein K10G9.1 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*

```

CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T23589; T24636
R.Mortimore, B.
Submitted to the EMBL Data Library, August 1994
A.Reference number: T23589
A.Accession: T23589
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-573 <M1>
A.Cross-references: UNIPROT:O09932; EMBL:E36282; PIDN:CAA85289.1; GSPDB:GN00021; CESP:KI0G9.1
A.Experimental source: clone KI0G9
R.Buck, D.
Submitted to the EMBL Data Library, February 1995
A.Reference number: Z19915
A.Accession: T24636
A>Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: DNA
A.Residues: 1-573 <M12>
A.Cross-references: EMBL:Z48055; PIDN:CAA8135.1; GSPDB:GN00021; CESP:KI0G9.1
A.Experimental source: clone T07A5
A.Gene: CESP:KI0G9.1
A.Map position: 3
A.Introns: 38/3; 87/3; 224/1; 272/3; 322/3; 444/3; 476/3; 496/1; 517/2

Query Match      32.7%; Score 971; DB 2; Length 573;
Best Local Similarity 43.5%; Pred. No. 9.5e-71;
Matches 197; Conservative 83; Mismatches 163; Indels 10; Gaps 5;

Oy      62 RYIAINSGISPGCSFGIRCNLGVAVSMANNSTTHRGHHVQKAPSMDEPVLGILH 121
      47 RMQILMLHFGFALSFGIRSNFGVAKNMNNFIDAY--EVEHKEFFMGTGEVMES 103
Oy      122 SFPMGYITQIPGGEFCQFANRVFGFAIVATSTLNLIPSAARVHGVCIYV---RIL 178
Db      104 SFFGYAASQIPAGVIAKFAPNKLFMLGILFASLNLVTVAICLNHFPTDIFVMVIGVM 163
Oy      179 QGLVEGVTPACHGIGWSWAPPLERSRLATTAFCGSYGAAVVAMPACVIVQSGMSVF 238
Db      164 QGLALGVCCYPMHGWKVMKMAPPLERSKLATTTFGASGVAVVGLPASAYLVSHSWSSTPF 223
Oy      239 YVYGSFGLFWLFWMLLVYESPALHPSISEERKTIIEALTESAKLMLPLTKESTPMRRF 298
Db      224 YVFGALGIWMSILMWVYSGTSPETHGYISAEKTYITEKVSVA--VKNMILLTLPLPMRDM 281
Oy      299 FTSMNVVAIIYANFCRSWTFYLLISOPDYEEVGFESIKGVASALPHLWMTIIVDIG 358
Db      282 MTSRTVAIIIIICSPFRSNSFFLLGNQULTYMKDVLHIDIKNSGLIATFPQGMCIYITLS 341
Oy      359 GQIADFLRSRRIMSTTNVRKLMNCGFGMEATLLLVGYSKSAIVSFLVAVFGSFA 418
Db      342 GQISDYLRSSGMSSTEAVRKSVNTFGFVEAVMLGCLAFVADPIYATVATFLIIACSGAV 401
Oy      419 ISGFVNVHLDIAPRASILNGISNGVGLSGNVCPIYGAANTKHKTRREWOYVFLIASLV 478
Db      402 LSGFVNVHFDIAPRAPILMGIANGLGAIAG-VGGIVTNSLT-YQNPBGQMOWEFLIASI 459
Oy      479 HVGVIYFGVAFASGEKOPWAPPEEEMSEKGFV 511
Db      460 DIFGIIFPLIPAKGDVLPWAPPEEKEETNEFV 492

RESULT 5
T24633
hypochemical protein T07A5.3 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjDate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T24633
R.Buck, D.
Submitted to the EMBL Data Library, February 1995
A.Reference number: Z19915
A.Accession: T24633
A>Status: preliminary; translated from GB/EMBL/DBJ

```

A:Molecule type: DNA
A:Residues: 1-544 <MIL>
A:Cross-references: UNIPROT:Q10046; EMBL:Z48055; PTDN:CAA88134.1; GSPDB:GN00021; CESP:T070
A:Experimental source: clone T07A5
C:Genetics:
A:Gene: CESP:T07A5.3
A:Map position: 3
A:Introns: 38/3; 87/3; 272/3; 322/3; 444/3; 476/3; 496/1; 517/2

Query Match 32.0%; Score 950; DB 2; Length 544;
Best Local Similarity 41.4%; Pred. No. 4,56-69;
Matches 208; Conservative 78; Mismatches 171; Indels 46; Gaps 9;

OY RYIIMSLGRCISFGICRNLGVAIYMNSTTHRGHVVOKAQSPDETYGLIHG 121
 :|::||::||::||::||::||::||::||::||::||::||::||::||
Db RMQIALHAHFQAISFGIRSNFCAKRMVNNFTDAYG--EVAHERFLMTGAEGMMES 103
 :|::||::||::||::||::||::||::||::||::||::||::||
OY SFPMGIVTQIOGGFCICKPFAARVFGEIAVATSTLMMLIPSAKVHYGCIVFYI---L 178
 ||::||::||::||::||::||::||::||::||::||::||::||
Db SFFYGAAASQTPAGVLAAPAKPAFNKKIFMLGIIVASFNNILSISNFHPHYDDIFNVAVQAV 163
 |::||::||::||::||::||::||::||::||::||::||::||
OY QGLVGVTVYPACHGWSKAPPLERSRLATTAFCGSYAGA VVAMPPLAGVLVOYSGMSVYF 238
 164 QGLAGLVLYPAHGWKFPAPLPLERSKLATTAFTGSSVGVTGULPASAYLVSHFSNSTPF 223
 :|::||::||::||::||::||::||::||::||::||::||::||
OY YVYGSFGIFWYLFWLLVSYESPALHPSISEEKRYIDAIGESAKLMPITKFSPTWRRE 298
 ||::||::||::||::||::||::||::||::||::||::||::||
Db YVFGVGVITWSLIWMYVSHSFETHGYISDDEKQVKTEKIDGVAVNKNSLT--TLPMRDM 281
 224 YVFGVGVITWSLIWMYVSHSFETHGYISDDEKQVKTEKIDGVAVNKNSLT--TLPMRDM 281
OY PTSMVYVATIVANFCGSKWTFYLLIIQPDYEFEYFGEISKGVLSALPHVMITIVPIG 358
 :|::||::||::||::||::||::||::||::||::||::||::||
Db MTSSAWMALICTCFCKSWGFPELLGNOLTYMKDVLDIKNSGFISISPPQGMCTVTLAT 341
 282 MTSSAWMALICTCFCKSWGFPELLGNOLTYMKDVLDIKNSGFISISPPQGMCTVTLAT 341
OY GOIADFLRSRIINSTTNVRKLANCGCFGMEATLLLVGYSHSKVAISFLVLAVFGSPA 418
 359 GOIADFLRSRIINSTTNVRKLANCGCFGMEATLLLVGYSHSKVAISFLVLAVFGSPA 418
Db GOLCYLRSGKMGKSTAARKSVTPGTVEAMMLGCLAFRDPIYIAVCIVACTGSGSV 401
 342 GOLCYLRSGKMGKSTAARKSVTPGTVEAMMLGCLAFRDPIYIAVCIVACTGSGSV 401
OY ISGFVNVHLDIAPRVASILMGISNGVGLSGMCPIIVGAN---TKKTRBEOYVFLI 474
 419 ISGFVNVHLDIAPRVASILMGISNGVGLSGMCPIIVGAN---TKKTRBEOYVFLI 474
 :|::||::||::||::||::||::||::||::||::||::||::||
Db LSGFVNVHEDIAPRVAPIILMGIANGLGAVAG-----VGGVNTVTVTQNPDGMKVFLL 455
 402 LSGFVNVHEDIAPRVAPIILMGIANGLGAVAG-----VGGVNTVTVTQNPDGMKVFLL 455
OY ASLVHYGVITPVGPVASGKQPWA-BPEB-----MBEEKGPFVGH 513
 475 ASLVHYGVITPVGPVASGKQPWA-BPEB-----MBEEKGPFVGH 513
Db AMAIDIFGITFPLFIKAGDVLFPWARBPBKETRFNEFVRMSIKVRSLSRKTRNRBGDTSY 515
 456 AMAIDIFGITFPLFIKAGDVLFPWARBPBKETRFNEFVRMSIKVRSLSRKTRNRBGDTSY 515
OY DOLAGSDSEMED----EABPP 531
 514 DOLAGSDSEMED----EABPP 531
Db EK--EBDEEMKPCSKKEVARAP 536
 516 EK--EBDEEMKPCSKKEVARAP 536

RESULT 6
S40767
hypothetical protein ZK512.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C:Accession: S40767
R:Hawkins, T.; Ainscough, R.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40759
A:Accession: S40767
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-466 <HAM>
A:Cross-references: UNIPROT:P34644; EMBL:Z22177
C:Genetics:
A:Introns: 21/2; 38/2; 109/3; 149/2; 188/3; 247/1; 292/3; 346/1; 376/3; 451/2
C:Keywords: transmembrane protein

Query Match 29.8%; Score 885; DB 2; Length 466;
Best Local Similarity 41.7%; Pred. No. 6,9e-64;
Matches 185; Conservative 75; Mismatches 140; Indels 44; Gaps 8;

OY KRLAGRALGKLRILEKRQGAGATTLISADGRVTTQTDRP--PVVDCTCFGLPR-RYI 64
 9 KRLAGRALGKLRILEKRQGAGATTLISADGRVTTQTDRP--PVVDCTCFGLPR-RYI 64

```
Db      12 KQWVEPLAKMTAAAAASATGAAPPOQOMQREGENENPMQHSNKVLQVMEQTWIGCKRKMTL 71
Qy      65 IAIMSGFCISFGIRCNLGVAVIVSVNNSTHRRGHVVVQKAQPSWDEPGLIHGSEF 124
Db      72 IAILANMGWMSFGIRCNFGAKKTHYKXVYDYPG--KVMHHEFWMTIDELSVESSTF 128
Qy      125 WGYIVTQIPGFCICQFAANRVFGPAIVTSTLMLIPSAARVHYG-CVIFVRILOGIVE 183
Db      129 YGVLVQTQIPAGFLAKFPENKLFSGFQIGVAFNLILLPYGFVKSDYLAIFIQIQGLVQ 188
Qy      134 GTTYPACGICGSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQVSGSSVFYVGS 243
Db      139 GVCYPMAGHVMRYMAPPMERSKLATTAFCGSYAGAVTGLPLSAFVSYVSMAPFLVXV 248
Qy      244 FGIYVFLVFLVSYSPALHPSISEERKYIEDAIGESAKLMNPLTKFSTPRRFTSP 303
Db      249 CGVIAWMLFCVTEFKPAHFPTISOBEKFIEDALGHVSN-THP-TLFLAYFNFFLEP 306
Qy      304 -----VYAIIV-----ANFCSWTFYLLISQPDYF 329
Db      307 AKVQNTMLNENFGIYQNPANIOKLIISVNNPAFKINNKFAFPARSMTFLLQNLQITVM 366
Qy      330 BEVFGFEISKVLVSALPHLVMTIIVPIGQIADFLRSRINSTNVKRLMCGGFQMEA 389
Db      367 KEALGKTIADSGLLAIPHVLVWGCVLWGGQLADYLRSNKILSTAVARKIFNCGFGGGBA 426
Qy      390 TLLLVGSHSGKVAISFLVAVG 413
Db      427 AFMLIVAYTSDTATMLIAVAG 450
```

RESULT 7

G88553
protein C38C10.2 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88553
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; PMID:99069613; and www_sanger.ac.uk/Projects/C_eleg
A>Note: see webdites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-493 <STO>
A:Cross-references: UNIPROT:Q03567; GB:chr_III; PIDN:CAA79549.1; PID:G3874873; GSPDB:GNC
C:Genetics:
A:Gene: C38C10.2
A:Map position: 3

Query Match 26.1%; Score 775.5; DB 2; Length 493;
Best Local Similarity 32.3%; Pred. No. 5, 6e-55;

Matches 163; Conservative 102; Mismatches 196; Indels 43; Gaps 9;

```
Qy      46 TRDPVVDDTCFGLRRRIYIAIMSGFCISFGIRCNLGVAVIVSVNNSTHRRGHVVVQ 105
Db      5 TTKPRLVST-----RFALSLVMEFGCLVTTMMRNMSFAVAVCWENKKTDTG---VE 54
Qy      106 K-----AQSMDPEYVGLIHGSEFMGVIYVQIPGFCICQFAANRVF 147
Db      55 KYSRCCKEMTPVESNSVIGFEDMDKQTGMWLSFFYIGSQIIGHLARSYGKRV 114
Qy      148 GFAIVATSTLNLIPSAARVHYGCVIFVRILOGIVEVTPYACGHSKMAPPLERSRLA 207
Db      115 FTIIGSALLTLNLPVPAARTSEVALALIRAAIGFGATFPAMHTWMSVWGPELISVLT 174
Qy      208 TTAFCGSYAGAVVAMPPLAGVLVQV---SGWSSVFYVYSGFQIFWYLFMLLVSYESALHP 264
Db      175 GVTYGAQQIGNVIVPLSGFLEYGFDGGMPSIFYIIGVGVLMTAVMVVYSSDKRATHP 234
```

```
Qy      265 SISEERKYIEDAIGESAKLMNPLTKF-STPMRRFTSPVYAIIVANFCRSWTFYLLI 323
Db      235 RITPEKQYIVAV--EASMGKDTGKVPSTPIKILITPAVACWAGFADGMYTMLV 292
Qy      324 SQPDYFEVFGFEISKVLVSALPHLVMTIIVPIGQIADFLRSRINSTNVKRLMNG 383
Db      293 SLPSFLKQVLGINTLSLQAVASIPYIAVFLAINAGVLAIDLRSGILSTLTRPAAMLV 352
Qy      334 GEGMEATLLLVGY--SSKGVASIFLVAVGSGFASGFPVNNHDIAPRYASILMGIS 441
Db      353 ALIIGQIFLVASGYCGCCQDVYIIFITCGMAISGLQYAGFVNVYLEIAPPSGVWNG 412
Qy      442 NGVTLSGMVCPIYVGMATKTRKREKQYVFLIASLVHYGVITYGVAPASGEKQWAE 501
Db      413 NITISLAGIISPAVSYLTLPNGTQEQWQVMLTAGIILITGALISIFASGEVQWMA--- 469
Qy      502 EMSEKCGFVGHQDLASGDDSEME 525
Db      470 KLTAE-----GHEMAPLREGEKIE 489
```

RESULT 8

S28286
hypothetical protein C38C10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Feb-1997
C:Accession: S28286
R:Thomas, K.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28285
A:Accession: S28286
A:Molecule type: DNA
A:Residues: 1-472 <THO>
A:Cross-references: EMBL:219153
C:Genetics:
A:Introns: 50/3; 287/3; 351/3; 412/3
A:Keywords: transmembrane protein

Query Match 25.7%; Score 763.5; DB 2; Length 472;
Best Local Similarity 33.1%; Pred. No. 5e-54;

Matches 158; Conservative 96; Mismatches 187; Indels 37; Gaps 8;

```
Qy      72 GFCISFGIRCNLGVAVIVSVNNSTHRRGHVVQK-----AQSMDP 113
Db      4 GCLVYTMKRTNMSFAVAVCWENKKTDTG---VEKYSRCCKEMTPVESNSVIGFEDMDK 59
Qy      114 ETVGLIHGSEFMGVIYVQIPGFCICQFAANRVFGPAIVTSTLMLIPSAARVHYGCVI 173
Db      60 QTTGMVLSFFYGYIGSQIIGHLARSYGKRVFVTLIGSLTLTLNFPVARTSEVALA 119
Qy      174 FVRILOGIVEVTPYACGHSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQV-- 231
Db      120 IIRAAIGFQCATFPAMHTWMSVWGPELISVLTGVTYAGAQIGNVIVPLSGFCEYOF 179
Qy      232 -SGWSSVFYVYSGFQIFWYLFMLLVSYESPALHPSISEERKYIEDAIGESAKLMNPLTK 290
Db      180 DCGMPSIFYIIGVFLVMTAVMVVYSSDKRATHPITPEKQYIVAV--EASMGKDTGK 237
Qy      291 F-STPMRRFTSPVYAIIVANFCRSWTFYLLIQPDYFEVFGFEISKVLVSALPHL 349
Db      238 VPSTPMIKILITPAVACWAGFADGMYTMLVSLPFLKQVLGINTLSLQAVASIPYI 297
Qy      350 VNTIIVPIGQIADFLRSRINSTNVKRLMNGCGFGMEATLLLVGY--SSKGVASIF 407
Db      298 AVFLAINAGVLAIDLRSGILSTLTRPAAMLVALIGGCIPLVASGYCGCCQDVYIIF 357
Qy      408 IVLAVGSGFASGFPVNNHDIAPRYASILMGISNGVTLSGMVCPIYVGMATKTRKTR 467
Db      356 ITCGMAISGLQYAGFVNVYLEIAPPSGVWGTGNTISLAGIISPAVSYLTLPNGTQ 417
Qy      468 WQYVFLIASLVHYGVITYGVAPASGEKQWAEPEMSEBEKCFVGHQDLASGDDSEME 525
Db      418 WQVLMLTAGIILITGALISIFASGEVQWMA---KLTAE-----GHEMAPLREGEKIE 468
```


Db 74 NMSPDIGIILLSTSTGYVIIIOVPVGFSGIYSTKMKIGFALCASSVSLIIPPAAGIGV 133
Qy 170 GCYIFVRIIOGLVEGVTPYPCAGIWSKMAPLERSLATTAFGSGYAGAVVMPAGVAV 229
Db 134 AMVVVCRAVOGAAGIIVARQPEIIVKMAPLERGLTSMSTGSPILGFFIIVLVGVIC 193
Qy 230 QYSGMSSVYVYVGSFGIFMYLFWLVSYPALHPSISEERKYLBDAGISAKLMPILT 289
Db 194 ESLGMPVYIFGACCAVCLLMFVLFYDDPKDHPICISISEKXYITSSIVQOVS----SS 249
Qy 290 KSTPMRRFPTSMRYAIIIVANPCRSWTYLLISQPDVFEVFGFELISKVLGVALPHL 349
Db 250 RQSLPKALKLPLVWALISIGSFTFWSHNMVLTYPFINSMLHVNIKENGFLSSLPYL 309
Qy 350 VMTIYPIGGQIADFLRSRIMSTTVKRLKMGCGFMEATLLLVGVGSHSKGVAL-SFL 408
Db 310 FAMICGNLAGQLSDFLTNNILSVIARVRLFTNAGLGLALIGVCLPYLSTFYSLVITL 369
Qy 409 VLAVGSFSAISGFVNVNHLDIAPRYASILMGISNGVGLSGVCPPIVGMATGKTRBEM 468
Db 370 ILAAGTSGFCLGCVFINGDIAPRYGFIKACSTLGMIGLHASTLTLGLIKODEBSAM 429
Qy 469 QYVFLIASLVHGVIFYGVFASGEGQPAEPEE 502
Db 430 EKTFLMAAINVTGLIFLYIVATVIAETIQWAKERQ 463

RESULT 12

869915
sodium-phosphate transport system 1 - mouse
C1:Species: Mus musculus (house mouse)
C1:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C1:Accession: S69915
R:Chong, S.S.; Kozak, C.A.; Liu, L.; Kristjansson, K.; Dunn, S.T.; Bourdeau, J.E.; Hughes
Am. J. Physiol. 268, 1038-1045, 1995
A>Title: Cloning, genetic mapping, and expression analysis of a mouse renal sodium-deper
A:Reference number: S69915
A:Accession: S69915
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-465 <CHO-
A:Cross-references: UNIPROT:Q61983; EMBL:X77241; NID:g887522; PIDD:CAA54459.1; PID:g8875

Query Match 20.8%; Score 619; DB 2; Length 465;
Best Local Similarity 31.5%; Pred. No. 2.6e-42;
Matches 141; Conservative 88; Mismatches 203; Indels 16; Gaps 6;
Qy 62 RYIIAMSGLGR--ISFGIRCNLGVAIYSVNNNS--TTRGGHVVYQKQ-----FSMD 112
Db 17 RYGLAIL--LHFCNTAIMAQRYCLNLTVMVANNNTGSPHLSNBSVVEMLDYNKPYVSW 74
Qy 113 PETVLIHGSFPMGYVITQIPGGFICQKFAANRVGFAIVATSTLMMLIPSAARYHGV 172
Db 75 PDIQGLISVFFGMYVVOAPVGYLSGIYPMKLISSLPSSLSMLLIPPAQYCALV 134
Qy 173 IFVRIIOGLVEGVTPYPCAGIWSKMAPLERSLATTAFGSGYAGAVVMPAGVAV 232
Db 135 IYCRVLQIAGIAGVTSQGEIHWKMAPLERGLTSMSTGSPILGFFIIVLVGVIC 194
Qy 233 GMSVYVYVYVGSFGIFMYLFWLVSYPALHPSISEERKYLBDAGISAKLMPILT 292
Db 195 GMPVYIFGIVGCVLISWFLFDPDPKHDPMSSEKDYIISIMQOAS-----SGROS 250
Qy 299 TPMRRFPTSMRYAIIIVANPCRSWTYLLISQPDVFEVFGFELISKVLGVALPHL 352
Db 251 LPIKAMLSLPLWAILNSFAIWSLSLVITPTISTVLHVNVKENGFLSSLPYL 310
Qy 353 IIVPIGGQIADFLRSRIMSTTVKRLKMGCGFMEATLLLVGVGSHSKGVALISFLVA 411
Db 311 ICGIAGQMSDFLIRKISIVYVRLFTLISFGCVIIMCLLYKSYNFYGVIFLTA 370
Qy 412 VGFSGFALSGFVNVNHLDIAPRYASILMGISNGVGLSGVCPPIVGMATGKTRBEM 471

Db 371 NSTLSFSGQILINALDIAPRYGFLKAVTALIGMFGGLISSTLAGILINDPEYAMHKI 430
Qy 472 FLIASLVHGVIFYGVFASGEGQPAE 499
Db 431 SFLMAGINVTCLVFFLPAKGEIQWAK 458

RESULT 13

139473
Na+-dependent phosphate cotransporter - human
C1:Species: Homo sapiens (man)
C1:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C1:Accession: U39473
R:Minamoto, K.; Tatsumi, S.; Sonoda, T.; Yamamoto, H.; Minami, H.; Taketani, Y.; Takeda,
Biochem. J. 305, 81-85, 1995
A>Title: Cloning and functional expression of a Na(+)-dependent phosphate co-transporter
A:Reference number: U39473; MUID:95126533; PMID:7826557
A:Accession: U39473
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-465 <RES>
A:Cross-references: UNIPROT:Q14916; GB:D28532; NID:6339841; PIDD:BA05888.1; PID:6639842

Query Match 20.8%; Score 616.5; DB 2; Length 465;
Best Local Similarity 29.7%; Pred. No. 4.1e-42;
Matches 135; Conservative 94; Mismatches 198; Indels 27; Gaps 5;

Qy 72 GFC-----ISFGIRCN-----NLGVAIYSVNNNS--TTRGGHVVYQKQ-----AQF 109
Db 12 GFCSSFRYGLSFLVHCNVIITRQMLCLNLTVMVANNNTGSPHLSNBSVVEMLDYNKPYV 71
Qy 110 SMDPFTVLIHGSFPMGYVITQIPGGFICQKFAANRVGFAIVATSTLMMLIPSAARYH 169
Db 72 NMSPDIGIILLSTSTGYVIIIOVPVGFSGIYSTKMKIGFALCASSVSLIIPPAAGIGV 131
Qy 170 GCYIFVRIIOGLVEGVTPYPCAGIWSKMAPLERSLATTAFGSGYAGAVVMPAGVAV 229
Db 134 AMVVVCRAVOGAAGIIVARQPEIIVKMAPLERGLTSMSTGSPILGFFIIVLVGVIC 191
Qy 230 QYSGMSSVYVYVGSFGIFMYLFWLVSYPALHPSISEERKYLBDAGISAKLMPILT 289
Db 194 ESLGMPVYIFGACCAVCLLMFVLFYDDPKDHPICISISEKXYITSSIVQOVS----SS 247
Qy 290 KSTPMRRFPTSMRYAIIIVANPCRSWTYLLISQPDVFEVFGFELISKVLGVALPHL 349
Db 248 RQSLPKALKLPLVWALISIGSFTFWSHNMVLTYPFINSMLHVNIKENGFLSSLPYL 307
Qy 350 VMTIYPIGGQIADFLRSRIMSTTVKRLKMGCGFMEATLLLVGVGSHSKGVAL-SFL 408
Db 308 FAMICGNLAGQLSDFLTNNILSVIARVRLFTNAGLGLALIGVCLPYLSTFYSLVITL 367
Qy 409 VLAVGSFSAISGFVNVNHLDIAPRYASILMGISNGVGLSGVCPPIVGMATGKTRBEM 468
Db 368 ILAAGTSGFCLGCVFINGDIAPRYGFIKACSTLGMIGLHASTLTLGLIKODEBSAM 427
Qy 469 QYVFLIASLVHGVIFYGVFASGEGQPAEPEE 502
Db 428 EKTFLMAAINVTGLIFLYIVATVIAETIQWAKERQ 461

RESULT 14

T01534
hypoosmotic protein A IgG05110.nm - Arabidopsis thaliana
C1:Species: Arabidopsis thaliana (mouse-ear cress)
C1:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
C1:Accession: T01534
R:Andrews, S.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of A. thaliana IgG05110.
A:Reference number: Z14347
A:Accession: T01534
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-413 <AND>
 A:Cross-references: UNIPROT:O23065; EMBL:AF013293; NID:g2252823; PID:g2252847
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 4
 A:Introns: 79/3; 115/3; 128/3; 200/3; 288/3; 331/3; 353/3; 382/1
 A:Note: A.1G005110.nm
 C:Superfamily: hexuronate transporter

Query Match 20.1%; Score 596.5; DB 2; Length 413;
 Best Local Similarity 30.7%; Fred. No. 1.5e-40;
 Matches 139; Conservative 62; Mismatches 133; Indels 119; Gaps 9;

QY 60 PRRYIIAIIISGIGFCISFGICRNLGVAIVSMVNNSTTRHGHHVVOQAQFSDEPTVGLI 119
 DB 59 PRRYIIAIIISGIGFCISFGICRNLGVAIVSMVNNSTTRHGHHVVOQAQFSDEPTVGLI 103
 QY 120 HGSFFMGVYIVTQIPGGFICQKPAANRVGFALVATSTLMMLIPSAARVHVCVIFVRIIQ 179
 DB 104 QSSFFMGVYIVTQIPGGFICQKPAANRVGFALVATSTLMMLIPSAARVHVCVIFVRIIQ 127
 QY 180 GLVEGVYTPACHGWSKAPPLERSRLATTAFCGAGAVVAMPPLAGLVVOYSGWSVIFY 239
 DB 128 --KGVAMPANNNMLSKWI PVSESRSLALVYSGWYLGSLVAPMLITKFGWPSVIFY 184
 QY 240 VYSGFIFMYLFMYLVSYSPALHPSISEERKYIEDAIGSAKLMNLTKESTPMRRFF 299
 DB 185 SFGISGWSFIMLMLKFAISSPDDBDLSEERKVI--LGGS-KREPVYI--PMKIL 238
 QY 300 TSMFYAIIIVANFCRSMTFYLLLSQPDYF-----EEVGFERISKVG 341
 DB 239 SKPVMALIIHFCNNMGTFFILLTMMPTVYNGARSSAVISLTFNIPCEQVLKPNLTESG 298
 QY 342 LVSLALPHLVMTIIVPIGQIADFLSRIMSTTNVTKLMNCGFGMEATLLLVGYSHSK 401
 DB 299 LLCVLPMLTMAVFNANIGMADTLVSRG-LSITN----- 331
 QY 402 GVAISPLVAVGSGFASISGNVNHLDIAPRYASITMGISNGVGLSGMVCPIIVGAMTK 461
 DB 332 -----GDAFSSQSGISXNHQDIGPRYAGVLLGSLNTAGVLAGVFGTAATGYLIQ 380
 QY 462 HKTREMOYVFLIASLVHYGVIFYGVFASGEK 494
 DB 381 ---RGSMDVFPKVAVALYLGIVVNLFPATGEK 410

RESULT 15

T45634
 hypothetical protein F13112.30 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C:Accession: T45634
 R:Choline, N.; Robert, C.; Brothier, P.; Wincker, P.; Catolico, L.; Artiguenave, F.; Sa
 submitted to the Protein Sequence Database, November 1999
 A:Reference number: Z23010
 A:Accession: T45634
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-537 <CHO>
 A:Cross-references: UNIPROT:Q9SD75; EMBL:AL133292
 A:Experimental source: cultivar Columbia; BAC clone F13112
 C:Genetics:
 A:Map position: 3
 A:Introns: 35/2; 153/3; 229/2; 350/3; 399/3; 445/3; 457/1
 A:Note: F13112.30

Query Match 15.9%; Score 471; DB 2; Length 537;
 Best Local Similarity 27.8%; Fred. No. 3.1e-30;
 Matches 141; Conservative 80; Mismatches 221; Indels 66; Gaps 12;
 QY 9 RKL---AGRALGKL-----HRLLEKRCGAGTLEISADGRPVTTQTRDP 50
 DB 47 RKLVLCTGRVYVNSLKFNTGNTSVDLGIPRHRLRVSCDARTPEETA-----AEITQPN 101

QY 51 VVDCFCGLPRYIIAIIISGIGFCISFGICRNLGVAIVSMVNNSTTRHGHHVVOQAQFS 110
 DB 102 FSE---FITSERVAVVAMALALALCNADRVVMAIVPL-----SLSG----- 143
 QY 111 WDEPTVGLIHGSPFWGYIVTQIPGGFICQKPAANRVGFALVATSTLMMLIPSAARVHYG 170
 DB 144 WKSFSFGIVQSSFLMGVLIISPIAGTILVDRYGVKVVAMGVAMLSLTFILPMADSSLM 203
 QY 171 CVTVRIIQLVEGVYTPACHGWSKAPPLERSRLATTAFCGAGAVVAMPPLAGLVVO 230
 DB 204 ALLARAVVGAEGVALPCNNNVAVRFPPTERRAVGIAVAGQLGNNVGLMILSPILMS 263
 QY 231 YSGWSVYVYVYVSGFIFMYLFMYLVSYSPALHPSISEERKYIEDAIGSAKLMN 286
 DB 264 QGGIYGPVYVIGLSGFLMLVMLSATSAAPRHHQITKSELEIYKQKQISTMENKRS- 322
 QY 287 PLTKFSTPMRRFPTSMFYAIIIVANFCRSMTFYLLLSQPDYFEEVGFERISKVGLVSAL 346
 DB 323 --TSGIPEFGRLLSKMPTMAIVANSMHSMVYHVN--KQAMF-----SAV 365
 QY 347 PHLVMTIIVPIGQIADFLSRIMSTTNVTKLMNCGFGMEATLLLVGYSHSKVAIS 406
 DB 366 PWSMAVFTGYIAGFWSDDL--IRGTSITLTKIMQSIGFIPGIALIGLTTAKQPLVASA 424
 QY 407 FLVAVGSGFASISGNVNHLDIAPRYASITMGISNGVGLSGMVCPIIVGAMTKHKTRE 466
 DB 425 WLSLAVGKSSSHLGFILNIDELAPERSGVHGMCLTAGTLAAVIG--TVGAGFFVELLG 482
 QY 467 EMQYVFLIASLVHYGVIFYGVFASGEK 494
 DB 483 SFGFILLTALVILLSALFNYIATGER 510

Search completed: June 2, 2005, 11:32:25
 Job time : 44 secs

THIS PAGE BLANK (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:19:52 ; Search time 178 Seconds
(without alignments)
1611.036 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEFRLKAGLALGKHL.....YGATHTSTPQPRPPPPVVDY 560

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2962	99.7	560	2	Q9P2U7 homo sapien
2	2953	99.4	560	2	Q6PCD0
3	2925	98.5	560	2	Q62634
4	2460	82.8	576	2	Q6INC8
5	2444	82.3	576	2	Q715L3
6	2338.5	78.7	584	2	Q8AM47
7	2317.5	78.0	582	2	Q9P2U8
8	2313.5	77.9	582	2	Q92087
9	2313.5	77.9	582	2	Q9J112
10	2308.5	77.7	582	2	Q8BLE7
11	2198	74.0	588	2	Q8K1Q1
12	2198	74.0	588	2	Q7TSF2
13	2185	73.6	589	2	Q8NDX2
14	2154.5	72.5	601	2	Q8BPU8
15	2107	70.9	402	2	Q7TQH3
16	1981	66.7	515	2	Q8JFT2
17	1358	45.7	592	2	Q7Q3R3
18	1297	43.7	576	1	Y006 CAEBL
19	1295.5	43.6	632	2	Q86P76
20	1294	43.6	563	2	Q9TZN7
21	1198.5	40.4	560	2	Q9VQC0
22	1051	35.4	201	2	Q8ZNR7
23	1020	34.3	544	2	Q7Q580
24	986.5	33.2	502	2	Q9VDM0
25	971	32.7	573	2	Q00932
26	950	32.0	544	1	VRT3 CAEBL
27	940	31.6	495	1	S175_HUMAN
28	931	31.3	495	1	S175_SHEEP
29	929	31.3	476	2	Q7Q579
30	927	31.2	495	1	S175_MOUSE
31	842	28.4	479	2	Q23514

32	798	26.9	533	2	Q7Q1S5	Q7Q1S5 anophelies g
33	798	26.9	559	2	Q9VYG7	Q9VYG7 dirosophila
34	787	26.5	955	2	Q7Q367	Q7Q367 anophelies g
35	775.5	26.1	493	1	Y1D2 CAEBL	Y1D2 CAEBL
36	774.5	26.1	535	2	Q7PMK4	Q7PMK4 anophelies g
37	767.5	25.8	529	1	PICO DROME	Q7PMK4 anophelies g
38	749	25.2	483	1	PICO DROME	Q61369 dirosophila
39	747	25.2	493	2	Q9VR44	Q9VR44 dirosophila
40	743.5	25.0	541	2	Q8GX78	Q8GX78 arabidopsis
41	742.5	25.0	591	2	Q652N5	Q652N5 oryza sativ
42	742.5	24.5	485	2	Q7PSC6	Q7PSC6 anophelies g
43	723.5	24.4	505	2	Q7QA73	Q7QA73 anophelies g
44	723.5	24.4	529	2	Q9SDI4	Q9SDI4 oryza sativ
45	720.5	24.3	512	2	Q82390	Q82390 arabidopsis

ALIGNMENTS

RESULT 1									
ID	Q9P2U7	PRELIMINARY;	PRT;	560 AA.					
AC	Q9P2U7								
DT	01-OCT-2000 (TREMBLrel. 15, Created)								
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)								
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)								
DE	Brain-specific Na-dependent inorganic phosphate cotransporter.								
GN	Name=BNPT;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	TISSUE=Brain;								
RX	MEDLINE=20281869; PubMed=10820226;								
RA	Alhara Y., Mashima H., Onda H., Hisano S., Kasuya H., Horii T., Yamada S., Tomura H., Yamada Y., Inoue I., Kojima I., Takeda J.;								
RT	"Molecular cloning of a novel brain-type Na(+)-dependent inorganic phosphate cotransporter.";								
RL	J. Neurochem. 74:2622-2625(2000).								
DR	EMBL; AB032436; BAA92875.1; -.								
DR	Gene; HGNC:16704; SLC17A7.								
DR	GO; GO:0016021; C:integral to membrane; TAS.								
DR	GO; GO:0015321; F:sodium-dependent phosphate transporter acti. . .; TAS.								
DR	GO; GO:0006817; P:phosphate transport; TAS.								
DR	InterPro; IPR007114; MPS.								
DR	PROSITE; PS50850; MPS; 1.								
SO	SEQUENCE 560 AA; 61613 MW; C88DAFB34B6E45B6 CRC64;								
Query Match									
Best Local Similarity 99.7%; Score 2962; DB 2; Length 560;									
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
QY	1	MEFRQEFRLKAGLALGKHLLEKROGATTELSADGRVTTQTRPPVVDCTCFGLP	60						
DB	1	MEFRQEFRLKAGLALGKHLLEKROGATTELSADGRVTTQTRPPVVDCTCFGLP	60						
QY	61	RRYIATMSGIFGFCISGIRCNLGVATVSVNNSITRHGHHVYQKQFSDPETVGLIH	120						
DB	61	RRYIATMSGIFGFCISGIRCNLGVATVSVNNSITRHGHHVYQKQFSDPETVGLIH	120						
QY	121	GSFPMGYIVTQIPGFCICQKFAANRVGFPAIVASTLMMLIPSAARVHYGCVIPRIIOG	180						
DB	121	GSFPMGYIVTQIPGFCICQKFAANRVGFPAIVASTLMMLIPSAARVHYGCVIPRIIOG	180						
QY	181	LVEGVTPACHGIGSKAPPLERSRLATTAFCGSGYAGVAVVMPAGVVOYSGMSVPEYV	240						
DB	181	LVEGVTPACHGIGSKAPPLERSRLATTAFCGSGYAGVAVVMPAGVVOYSGMSVPEYV	240						
QY	241	YGSFGIFWYLFWLVSVESPALHPSISEBERKYIEDAIGESAKLMPLTKESTPWRREF	300						
DB	241	YGSFGIFWYLFWLVSVESPALHPSISEBERKYIEDAIGESAKLMPLTKESTPWRREF	300						

QY 301 SMPVVAIIYANCRSWTFFYLLISQPDYEEVFGFEISVGLVSALPHLWMTIIVPIGQ 360
 DB 301 SMPVVAIIYANCRSWTFFYLLISQPAYEEVFGFEISVGLVSALPHLWMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVRKLMNCGFGMEATLLVVGYSKVAISFLVAVGSGFAIS 420
 DB 361 IADFLRSRIMSTNVRKLMNCGFGMEATLLVVGYSKVAISFLVAVGSGFAIS 420
 QY 421 GENVNHLDIAPRYASIIIMGINSVGTLSGWCPIIVGAMTKHKTREEMQYVELIASLVHY 480
 DB 421 GENVNHLDIAPRYASIIIMGINSVGTLSGWCPIIVGAMTKHKTREEMQYVELIASLVHY 480
 QY 481 GGVIFGVYFASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
 DB 481 GGVIFGVYFASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
 QY 541 YGATHSTFQPPRPVPRDY 560
 DB 541 YGATHSTFQPPRPVPRDY 560

RESULT 2

QY 06PCD0 PRELIMINARY; PRT; 560 AA.
 AC 06PCD0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Solute carrier family 17, member 7.
 GN Name:SLC17A7;
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schen J.E.,
 RA Jones S.J., Matra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX Strausberg R.;
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC059379; AAH59379.1; -
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR PROSITE: PS00850; MFS; 1.
 SQ SEQUENCE 560 AA; 61672 MW; 928C45B0286E45B5 CRC64;

Query Match 99.4%; Score 2953; DB 2; Length 560;

Best Local Similarity 99.6%; Pred. No. 9,1e-214; Matches 558; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEFRQEFKRLAGRALGKHLRLERKOGAETLLEADGRPVYTTQTRDPVVDCTCFGLP 60
 DB 1 MEFRQEFKRLAGRALGKHLRLERKOGAETLLEADGRPVYTTQTRDPVVDCTCFGLP 60
 QY 61 RRYIIAIMGSGFCISFGIRCNLGVAVISVNNSTTRRGHVVOKAOSWDPVEVGLIH 120
 DB 61 RRYIIAIMGSGFCISFGIRCNLGVAVISVNNSTTRRGHVVOKAOSWDPVEVGLIH 120
 QY 121 GSFFMGVYVTOIPGFTICQKFAHNVFGFALVISTLNNLPSARVHGVCFVRIILOG 180
 DB 121 GSFFMGVYVTOIPGFTICQKFAHNVFGFALVISTLNNLPSARVHGVCFVRIILOG 180
 QY 181 LVEGVTYACGHSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGLVVQYSGMSVFFV 240
 DB 181 LVEGVTYACGHSKMAPLERSRLATTAFCGSYAGAVVAMPPLAGLVVQYSGMSVFFV 240
 QY 241 YGSPGIFWYLFWLLVSYSPALHPSISEERKYIEDAIGESAKLNNPLTKESTPMRRPFT 300
 DB 241 YGSPGIFWYLFWLLVSYSPALHPSISEERKYIEDAIGESAKLNNPLTKESTPMRRPFT 300
 QY 301 SMPVVAIIYANCRSWTFFYLLISQPDYEEVFGFEISVGLVSALPHLWMTIIVPIGQ 360
 DB 301 SMPVVAIIYANCRSWTFFYLLISQPAYEEVFGFEISVGLVSALPHLWMTIIVPIGQ 360
 QY 361 IADFLRSRIMSTNVRKLMNCGFGMEATLLVVGYSKVAISFLVAVGSGFAIS 420
 DB 361 IADFLRSRIMSTNVRKLMNCGFGMEATLLVVGYSKVAISFLVAVGSGFAIS 420
 QY 421 GENVNHLDIAPRYASIIIMGINSVGTLSGWCPIIVGAMTKHKTREEMQYVELIASLVHY 480
 DB 421 GENVNHLDIAPRYASIIIMGINSVGTLSGWCPIIVGAMTKHKTREEMQYVELIASLVHY 480
 QY 481 GGVIFGVYFASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
 DB 481 GGVIFGVYFASGEKQPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPGAPAPAPPS 540
 QY 541 YGATHSTFQPPRPVPRDY 560
 DB 541 YGATHSTFQPPRPVPRDY 560

RESULT 3

QY 062634 PRELIMINARY; PRT; 560 AA.
 AC 062634;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE Brain specific Na+-dependent inorganic phosphate cotransporter.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94261635; PubMed=8202535;
 RA Ni B., Rosteck P.R., Nadi N.S., Paul S.M.,
 RT "Cloning and expression of a cDNA encoding a brain-specific Na(+)-
 dependent inorganic phosphate cotransporter";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5607-5611(1994).
 DR EMBL: U07609; AAA19646.1; -
 DR PIR: I59302; I59302.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR PROSITE: PS00850; MFS; 1.
 SQ SEQUENCE 560 AA; 61665 MW; F686889F606B8305 CRC64;

Query Match 98.5%; Score 2925; DB 2; Length 560;

Best Local Similarity 98.2%; Pred. No. 1.2e-211;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEFOEERKLAGRAGLHRLERKOGAETLELSADGRPTVOTRPPVDDCTCFGLP 60
DB 1 MEFOEERKLAGRAGLHRLERKOGAETLELSADGRPTVOTRPPVDDCTCFGLP 60
QY 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISVWNNSTTHRGHVVOKQAFSPDETVGLIH 120
DB 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISVWNNSTTHRGHVVOKQAFSPDETVGLIH 120
QY 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFALVATSTLMLIPSAARVHYGCVIFVRILOG 180
DB 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFALVATSTLMLIPSAARVHYGCVIFVRILOG 180
QY 181 LVEGVTPACHGINSKMAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
DB 181 LVEGVTPACHGINSKMAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
QY 241 YGSGIFFWLFWLVSYSPPALHPSISEERKYLEDAIGESAKLMNPLTKSTPWRPFT 300
DB 241 YGSGIFFWLFWLVSYSPPALHPSISEERKYLEDAIGESAKLMNPLTKSTPWRPFT 300
QY 301 SMPYVAIVANFCRSWTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWNTIIVPIGQ 360
DB 301 SMPYVAIVANFCRSWTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWNTIIVPIGQ 360
QY 361 IADFLRSRRIMSTNVKRLNMGCGFMEATLLLVGSHSGVAVISFLVAVGSGPAIS 420
DB 361 IADFLRSRRIMSTNVKRLNMGCGFMEATLLLVGSHSGVAVISFLVAVGSGPAIS 420
QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMCPIIVGAMTHGKREEMQVFLASIVHY 480
DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGMCPIIVGAMTHGKREEMQVFLASIVHY 480
QY 481 GGVIFYGVFASGEQPAPEPEMSEBEKGFVGHQDLASDSEMEDAEPGAPAPAPPS 540
DB 481 GGVIFYGVFASGEQPAPEPEMSEBEKGFVGHQDLASDSEMEDAEPGAPAPAPPS 540
QY 541 YGATHSTFQPPPPPPVVDY 560
DB 541 YGATHSTFQPPPPPPVVDY 560

RESULT 4
Q6INC8 PRELIMINARY; PRT; 576 AA.
AC Q6INC8: 05-JUN-2004 (TREMBlrel. 27, Created)
DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
DE MG83509 protein.
GN Name=MG83509;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xeropodinae; Xenopus.
OX NCBI_TaxID=8355;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stepien L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Frange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.,
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative".
RL Dev. Dyn. 225:384-391(2002).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Klein S., Strausberg R.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC072355; AA072355.1; -.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005215; P:transporter activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR007114; MPS.
DR PROSITE: PS00850; MPS; 1.
SQ SEQUENCE 576 AA; 63905 MW; 93C2157CFB15CB62 CRC64;

Query Match 82.8%; Score 2460; DB 2; Length 576;
Best Local Similarity 83.6%; Pred. No. 1.2e-176;
Matches 459; Conservative 44; Mismatches 38; Indels 8; Gaps 2;

QY 1 MEFOEERKLAGRAGLHRLERKOGAETLELSADGRPTVOTRPPVDDCTCFGLP 60
DB 1 MEFOEERKLAGRAGLHRLERKOGAETLELSADGRPTVOTRPPVDDCTCFGLP 60
QY 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISVWNNSTTHRGHVVOKQAFSPDETVGLIH 120
DB 61 RRYIIAIVMSGLGFCISFGIRCNLGVAVISVWNNSTTHRGHVVOKQAFSPDETVGLIH 120
QY 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFALVATSTLMLIPSAARVHYGCVIFVRILOG 180
DB 121 GSFPMGYIVTQIPGGFICQKFAANRVFGFALVATSTLMLIPSAARVHYGCVIFVRILOG 180
QY 181 LVEGVTPACHGINSKMAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
DB 181 LVEGVTPACHGINSKMAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
QY 241 YGSGIFFWLFWLVSYSPPALHPSISEERKYLEDAIGESAKLMNPLTKSTPWRPFT 300
DB 241 YGSGIFFWLFWLVSYSPPALHPSISEERKYLEDAIGESAKLMNPLTKSTPWRPFT 300
QY 301 SMPYVAIVANFCRSWTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWNTIIVPIGQ 360
DB 301 SMPYVAIVANFCRSWTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWNTIIVPIGQ 360
QY 361 IADFLRSRRIMSTNVKRLNMGCGFMEATLLLVGSHSGVAVISFLVAVGSGPAIS 420
DB 361 IADFLRSRRIMSTNVKRLNMGCGFMEATLLLVGSHSGVAVISFLVAVGSGPAIS 420
QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGMCPIIVGAMTHGKREEMQVFLASIVHY 480
DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGMCPIIVGAMTHGKREEMQVFLASIVHY 480
QY 481 GGVIFYGVFASGEQPAPEPEMSEBEKGFVGHQDLASDSEMEDAEPGAPAPAPPS 540
DB 481 GGVIFYGVFASGEQPAPEPEMSEBEKGFVGHQDLASDSEMEDAEPGAPAPAPPS 540
QY 541 YGATHSTFQ 549
DB 541 YGATHSTFQ 549

Db 533 YGATQTTSQ 541

```
RESULT 5
Q715L3 PRELIMINARY; PRT; 576 AA.
ID 0715L3;
AC 0715L3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
DE Glutamate transporter.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=2915319; DOI=10.1016/S1567-133X(03)00057-7;
RA Gleason K.K., Donnelly V.R., Hela H.L.J., Cochran E.R.,
RA Gumalak-Smith J., Sana M.S.;
RT "The vesicular glutamate transporter 1 (xvGlut1) is expressed in
RT discrete regions of the developing Xenopus laevis nervous system.";
RL Gene Expr. Patterns 3:503-507(2003).
DR EMBL, AF548627; ANQ12345.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS. 1.
SQ SEQUENCE 576 AA; 63919 MW; 9262CA07FA4A49D1 CRC64;
```

Query Match 82.3%; Score 2444; DB 2; Length 576;
Best Local Similarity 84.0%; Pred. No. 2e-175;
Matches 461; Conservative 37; Mismatches 43; Indels 8; Gaps 2;

```
QY 1 MEFROEERKLAGALGKHLRLKROEGATLELSADGRPTVTTQTRDPVVDCTCGLR 60
DB 1 MEFROEERKLAGALGKHLRLKROEGATLELSADGRPTVTTQTRDPVVDCTCGLR 60
QY 61 RRYIIMSGLGFICISFGICRNGLVAIVSMNNSTHRRGGHVVV-OKAOPSWDETVGLHG 120
DB 61 RRYIIMSGLGFICISFGICRNGLVAIVSMNNSTHRRGGHVVV-OKAOPSWDETVGLHG 120
QY 121 GSFPMGYIVTQIPGGITCQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFVAILQGL 180
DB 121 GSFPMGYIVTQIPGGITCQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFVAILQGL 180
QY 181 LVEGVTPACHGIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSSVFYV 240
DB 181 LVEGVTPACHGIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSSVFYV 240
QY 241 YGSFGLFWLFWMLLVYESPALHPSISEERKYTEAIGESAKLMLPLKFSPPMRPFT 300
DB 241 YGSFGLFWLFWMLLVYESPALHPSISEERKYTEAIGESAKLMLPLKFSPPMRPFT 300
QY 301 SMPVVAIIYANFCRSWTFYLLISQPDYEEVGFESISKVGLVSALPHLWMTIIVIGQI 360
DB 301 SMPVVAIIYANFCRSWTFYLLISQPDYEEVGFESISKVGLVSALPHLWMTIIVIGQI 360
QY 361 IADFLRSRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGPAIS 420
DB 361 IADFLRSRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGPAIS 420
QY 421 GFNVNHLDIAPRYASTILMGISNGVGLTSGMVCPIYGAHTKHKTRREMOYVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASTILMGISNGVGLTSGMVCPIYGAHTKHKTRREMOYVFLIASLVHY 480
QY 481 GGVIFGVASGEKQWAPPEEMSEKCGFVGHIDQLAGSDSEMEDEAPPGAPAPPPPS 540
DB 481 GGVIFGVASGEKQWAPPEEMSEKCGFVGHIDQLAGSDSEMEDEAPPGAPAPPPPS 540
QY 541 YGATHTSTFQ 549
```

Db 533 YGATQTTSQ 541

```
RESULT 6
Q8AM47 PRELIMINARY; PRT; 584 AA.
ID 08AM47;
AC 08AM47;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Si-PAKCT73.2 (Novel protein similar to human solute carrier family 17
DE (Sodium-dependent inorganic phosphate cotransporter), member 6
DE (SLC17A6)).
GN Name=Si-PAKCT73.2;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL627170; CAD52142.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS50850; MFS. 1.
SQ SEQUENCE 584 AA; 64122 MW; 91C140D929EB85DB CRC64;
```

Query Match 78.7%; Score 2398.5; DB 2; Length 584;
Best Local Similarity 80.3%; Pred. No. 1.7e-167;
Matches 436; Conservative 47; Mismatches 55; Indels 5; Gaps 2;

```
QY 3 FROEERKLAGALGKHLRLKROEGATLELSADGRPTVTTQTRDPVVDCTCGLR 62
DB 10 FKEGKQLAGKTLGHVVRVIEKQPKBNIELTDEGRPAQINERKAPLDCCTCGLRPR 69
QY 63 YIIAIMSGLGFICISFGICRNGLVAIVSMNNSTHRRGGHVVV-OKAOPSWDETVGLHG 121
DB 70 YIIAIMSGLGFICISFGICRNGLVAIVSMNNSTHRRGGHVVV-OKAOPSWDETVGLHG 129
QY 122 SFFPMGYIVTQIPGGITCQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFVAILQGL 181
DB 130 SFFPMGYIVTQIPGGITCQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFVAILQGL 189
QY 182 VEGVTPACHGIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSSVFYV 241
DB 190 VEGVTPACHGIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSSVFYV 249
QY 242 GSFGLFWLFWMLLVYESPALHPSISEERKYTEAIGESAKLMLPLKFSPPMRPFTS 301
DB 250 GSFGLFWLFWMLLVYESPALHPSISEERKYTEAIGESAKLMLPLKFSPPMRPFTS 309
QY 302 MEVVAIIYANFCRSWTFYLLISQPDYEEVGFESISKVGLVSALPHLWMTIIVIGQI 361
DB 310 MEVVAIIYANFCRSWTFYLLISQPDYEEVGFESISKVGLVSALPHLWMTIIVIGQI 369
QY 362 ADFLRSRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGPAISG 421
DB 370 ADFLRSRIMSTTNVRKLMNCGFGMEATLLIVGYSHSKGVAISFLVLAVGFSGPAISG 429
QY 422 GFNVNHLDIAPRYASTILMGISNGVGLTSGMVCPIYGAHTKHKTRREMOYVFLIASLVHY 481
DB 430 GFNVNHLDIAPRYASTILMGISNGVGLTSGMVCPIYGAHTKHKTRREMOYVFLIASLVHY 489
QY 482 GVIIFGVASGEKQWAPPEEMSEKCGFVGHIDQLAGSDSEMEDEAPPGAPAPPPPSY 541
DB 490 GVIIFGVASGEKQWAPPEEMSEKCGFVGHIDQLAGSDSEMEDEAPPGAPAPPPPSY 545
QY 542 GAT 544
```


DB 546 GAT 548

RESULT 7

Q9P2U8 PRELIMINARY; Prt: 582 AA.

ID Q9P2U8 01-OCT-2000 (TREMBlRel. 15, Created)

AC Q9P2U8; 01-OCT-2000 (TREMBlRel. 15, Last sequence update)

DT 01-OCT-2000 (TREMBlRel. 15, Last annotation update)

DT 25-OCT-2004 (TREMBlRel. 28, Last annotation update)

DE Differentiation-associated Na-dependent inorganic phosphate

DE cotransporter (Differentiation-associated Na-dependent inorganic phosphate cocr).

GN Name=DMP1; Synonyms=SLC17A6;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain thalamus;

RX MEDLINE=20281869; PubMed=10820226;

RX Aithara Y., Maahia H., Onda H., Hisano S., Kasuya H., Hori T., Yamada S., Tomura H., Yamada Y., Inoue I., Kojima I., Takeda J.;

RT "Molecular cloning of a novel brain-type Na(+)-dependent inorganic phosphate cotransporter.";

RT J. Neurochem. 74:2622-2625(2000).

[2]

RP SEQUENCE FROM N.A.

RP TISSUE=PCR rescued clones;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L., Stadelman M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrincci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwen P.J., McKernan K.J., Malek U.A., Gunatirane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalios D.E., Schermer A., Schein J.E., Jones S.J., Warr M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3]

RP SEQUENCE FROM N.A.

RP TISSUE=PCR rescued clones;

RC Director MGC Project;

RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.

RL EMBL; AB032435; BAA92874.1; -

DR EMBL; BC069629; AAH69629.1; -

DR EMBL; BC069640; AAH69640.1; -

DR EMBL; BC069646; AAH69646.1; -

DR GeneW; HGNC:16703; SLC17A6.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPRO07114; MFS.

DR PROSITE; PS00850; MFS; 1.

SO SEQUENCE 582 AA; 64392 MW; CE761556FA18C6AD CRC64;

Query Match 78.0%; Score 2317.5; DB 2; Length 582;

Best Local Similarity 79.4%; Pred. No. 6.6e-166;

Matches 429; Conservative 56; Mismatches 50; Indels 5; Gaps 2

Oy		QOEFRRLARAPLAKGLHRLLEKXOQEAETLELSAOCRPPTTGTQRPVPVDCFCFLPARYI	64
Dd		13 KEGKLPRFAGSJAQYIRLVLEKKQDDGETTELTEDEOKPLEWPERKAPLCDCTCFELPARYI	72
Oy		65 IAIMSGLGFCISIGSRICNLGVALIVSMVNNSSTTHRGHVWQAOKOPSMDPETVLIHGSFF	124
Dd		73 IAIMSLGFGCISIGSRICNLGVALIVDMVNNSITHHGKVITKEKAFKNNDPELVGMIHGSFF	132
Oy		125 WGYIVTQIPGGFI CQKFAANRVFEGALVATSTLMMLIPSARVHYGCIVIFRILIOGLEVEG	184
Dd		133 WGYIIQTQIPGGYIASRLAANRVFGAAIILLTSTLMMLIPSAARVHYGCIVIFRILIOGLEVEG	192
Oy		185 VTYYPACHGIMSKAPLPERSRLATAFCGYSVAGAVVMAPLAGVLYVCGMSSVFYVYGSF	244
Dd		193 VTYYPACHGIMSKAPLPERSRLATTFSFGCSAGAIAMPLAGLIIVOTGHSSVFYVYGSF	252
Oy		245 GIFYWYLFWLLVSYESPALHPISISEEERXYIEDAIGESAKMLNPLTKSTWRREFTSMPV	304
Dd		253 GMVWVWFVLLVSYPSPAKHPITITDBERRYIEESIGESANLLIGAMEKFKTPMRKFTSMPV	312
Oy		305 YALIIVANPCRSWTFYLLILI SQPDYEEVYFGEISKVGLVSLPHLVNTTIIVPIGGQIADF	364
Dd		313 YALIIVANPCRSWTFYLLILIS QPAEEYEEVFEIGEISKVGLVASPHLVNTTIIVPIGGQIADF	372
Oy		365 LRSRRLRMTTNTRKLMNCGCFMEKMTLLLVYGSXSGVALISFYLVAVGSFGAISGFENV	424
Dd		373 LRSQRLLSTTTYYARKLMNCGGFMEKMTLLLVYGSYSTRGVALISFYLVAVGSFGAISGFENV	432
Oy		425 NHHDIAPRASILIMGINSVGTLISGMVCPIIVGANTHKHTKEEMQVYFLIALVHYGVLI	484
Dd		433 NHHDIAPRASILIMGINSVGTLISGMVCPIIVGANTKKSSEBQVYFLIALVHYGVLI	492
Oy		485 FYGVFASGERKOPWABEEPMESEBKCGFVGHDLAAGSDSEMEDAEAPPGAPAPPSPSYGAT	544
Dd		493 FYAIFASGERKOPWADBEETSEBKCGFIHEDEL----DETGDITQ-NVYNVTGTSYGAT	547
<hr/>			
RESULT 8			
ID	0920B7	PRELIMINARY;	PRT; 582 AA.
AC	0920B7;		
DT	01-DEC-2001 (TREMBLrel. 19, Created)		
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)		
DT	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
Dd	vesicular glutamate transporter 2 (Solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 6).		
GN	Name=slc17a6;		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCB1_TaxId=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
EX	MEDLINE=2143279; PubMed=11432869; DOI=10.1074/jbc.M104578200;		
RA	Bai L., Xu H., Collins J.F., Ghashan F.K.;		
RT	"Molecular and functional analysis of a novel neuronal vesicular		
RT	glutamate transporter.";		
RL	J. Biol. Chem. 276:36764-36769 (2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Eye;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Straubeberg R.L., Feingold B.A., Groupe L.H., Derge U.G.		
RA	Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,		
RA	Alschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,		
RA	Diatchenko L., Marutsuna K., Farmer A.A., Rubin G.W., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carlinini P., Prange C.,		
RA	Raina S.R., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Boak S.A., McMan P.J., McMernan K.J., Malek U.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Huliy S.W.,		
RA	Villation D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:665-680 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RX MEDLINE=20539913; PubMed=11076861; DOI=10.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multiplexed sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozawa T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tanaka A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
 RN EMBL; AK054549; BAC32349.1; -.
 DR MGD; MGI:2156052; Slc17a6.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0008021; C:synaptic vesicle; IDA.
 DR GO; GO:0005313; P:L-glutamate transporter activity; IDA.
 DR GO; GO:0001504; P:neurotransmitter uptake; IDA.
 DR InterPro; IPR007114; MFS.
 DR PROSITE; PS50850; MFS; 1.
 SQ SEQUENCE 582 AA; 64560 MW; 9P7A47C0B0C7A64D CRC64;

Query Match 77.7%; Score 2308.5; DB 2; Length 582;

Best Local Similarity 79.1%; Pred. No. 3.2e-165;
 Matches 427; Conservative 58; Mismatches 50; Indels 5; Gaps 2;
 QY 5 QEBRKLAGRALGKHLRLERKQGAETLELSADGRPTTTRDPVVDCTCFGLPRRYI 64
 DB 13 KEGKNFAGKSLGGIYRLERKQDNREITELTEGKPLEVEBKAPLDCCTCFGLPRRYI 72
 QY 65 IAINSGAGFCISFGIRCLGVAIVSMVNNSTTHRGHGVVVOKAQSPMDPEVTGLHSGFF 124
 DB 73 IAINSGAGFCISFGIRCLGVAIVDMVNNSTTHRGHGVVVOKAQSPMDPEVTGLHSGFF 132
 QY 125 WGYITVQIPGCFIQKPAANEVFGAIVATSTLNNLIPSAARVHYGCVIPVRIIQLVEG 184
 DB 133 WGYITVQIPGCVIYASRLAANVFGAAILLSTLNNLIPSAARVHYGCVIPVRIIQLVEG 192
 QY 185 VTPYACGIGSKMAKPLERSLATTAPFGSYAGAVVAMPGLCVLYVSGMSVFFVYGSF 244
 DB 193 VTPYACGIGSKMAKPLERSLATTAPFGSYAGAVVAMPGLCVLYVSGMSVFFVYGSF 252
 QY 245 GIPWYLPWLVSYSPALHPISIEERKYIEDAIGESAKLNNPLTKFSTPMRRPFTSNPV 304
 DB 253 GMYWTFWLVSYSPALHPITTDERRYIESIGESANLIGAMEKFTPMRKFTSNPV 312
 QY 305 YAIIVANFCSMTYLLILISQPDYFEVYFGEISKVLVSALPHLWMTIIVPIGQIDAF 364
 DB 313 YAIIVANFCSMTYLLILISQPAFBEVYFGEISKVLVSALPHLWMTIIVPIGQIDAF 372
 QY 365 LRSRRINSTVNRKLMNCGFGMEATLLVYGSKQVAISFLVLANGFSGFAISGRNV 424
 DB 373 LRSKQISTTVVRKIMNCGFGMEATLLVYGSHTRVASIFVLAVFGSFAISGRNV 432
 QY 425 NHDLPAPYASILMGISGVGTLSGMVCPITVGMATKHKREEMQYVLASLVHYGCVI 484
 DB 433 NHDLPAPYASILMGISGVGTLSGMVCPITVGMATKHKREEMQYVLASLVHYGCVI 492
 QY 485 FYGVFASGEKOPMAPEEMSESEKCFVGHQDLASDSEMEDEAPPAAPPSPSYGAT 544
 DB 493 FYALFASGEKOPMAPEEMSESEKCFIHEDEL----DETQDITQ-NVINGTTMSYCAT 547

RESULT 11
 ID 08K101 PRELIMINARY; PRT; 588 AA.
 AC 08K101.
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Vesicular glutamate transporter 3.
 GN Name=vglut3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague Dawley; TISSUE=Brain;
 RX MEDLINE=22092356; PubMed=12097496;
 RA Gras C., Herzog E., Belenchi G.C., Bernard V., Ravassard P., Pohl M.,
 RA Gaenier B., Girod B., El Westikawy S.;
 RT "A third vesicular glutamate transporter expressed by cholinergic and
 RT serotonergic neurons.";
 RL J. Neurosci. 22:5442-5451 (2002).
 RN EMBL; AJ491795; CAD37138.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR007114; MFS.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR PROSITE; PS50850; MFS; 1.
 SQ SEQUENCE 588 AA; 64754 MW; 9644C021D94286B5 CRC64;

Query Match 74.0%; Score 2198; DB 2; Length 588;

Best Local Similarity 76.9%; Pred. No. 6.7e-157;
Matches 415; Conservative 50; Mismatches 69; Indels 6; Gaps 3;

```
OY 5 OEEFKLAGRALGKHLRLLEKROEGAEITLISADGPVTTQTRDPVVDCTCGFLPRRYI 64
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 18 KEGVANAAGDSIGILQKRLDGTNEGDAIELSEBRPVQTSARAPVDCSCCGIPKRII 77
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 65 IAIMSGLGFCISFGIRCNLGVAVISVMNNSTTHRGHVAVVQAKQSPDETYGLIHGSPF 124
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 78 IAVMSGLGFCISFGIRCNLGVAVIVEMNNSTYVQKPEIQTAQFNMPDETYGLIHGSPF 137
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 125 WGIYVTOIPGGFTICQKPAANRVFGAIVATSTLNMIPSAARVHGCIVFVRILOGLVHG 184
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 138 WGIYVTOIPGGFTISNKPFAANRVFGAIVATSTLNMIPSAARVHGCIVFVRILOGLVHG 197
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 185 VTPYPAHGIMSKWAPLERSRLATTAFGGSYAGAVVAMPAGLVLYOYSGMSSVFYVYGSF 244
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 198 VTPYPAHGIMSKWAPLERSRLATTAFGGSYAGAVVAMPAGLVLYOYSGMSSVFYVYGSF 257
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 245 GTFWTLFWLIVSYESPALHPISISEBRKYIEDAIGESAKLNPITKFTSPMRFFTSMPV 304
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 256 GIWMFMFLQAYECGAVHPTISNEERTYIETISIGGANLAS-LSKFTPMWRFFTSLPV 316
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 305 VAIIVANPCRSWTFYLLISQPDYFEVFGFEISKVGLVSALPHLVMTIIVPIGQIADF 364
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 317 VAIIVANPCRSWTFYLLISQPAYFEVFGFAISKVGLLSAVPHVMWMTIIVPIGQIADY 376
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 365 LRSRRIMSTTVNRKILMNCGFGMEATLLLVGYSHSKGVAISFLVAVGFSGFAISGFNV 424
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 377 LRSRILITTTAVARKILMNCGFGMEATLLLVGFSHTKGVAISFLVAVGFSGFAISGFNV 436
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 425 NMLDIAPRASILMISNGVGLTSGMVCPIVGMATKTKTREEMQVYFLIALVHYSGVI 484
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 437 NMLDIAPRASILMISNGVGLTSGMVCPLIVGAMTKTKTREEMQVYFLIALVHYSGVI 496
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 485 FYGVASGEKQWAPBEEMSEKCGFVGHDLAAGSDSDSEMEDBAPPGAPAPPPSYGAT 544
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 497 FYGVASGEKQWAPBEEMSEKCGIITDDELA--EETELNHEA--FVSPKKMSYGAT 551
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

RESULT 12

```
OYTSF2 PRELIMINARY; PRT; 588 AA.
AC OYTSF2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Vesicular glutamate transporter 3.
GN Name=Vglut3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Fremean R.T. Jr., Butman J.L., Qureshi T., Tran C.H., Proctor J.,
RA Johnson J., Zhang H., Sulzer D., Copenhagen D.R., Storm-Mathisen J.,
RA Reiner R.U., Chaudhry F.A., Edwards R.H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117026; AAM50094.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00850; MFS; 1.
SQ SEQUENCE 588 AA; 64768 MW; 97B1A5801D272684 CRC64;
```

Query Match 74.0%; Score 2198; DB 2; Length 588;
Best Local Similarity 76.9%; Pred. No. 6.7e-157;
Matches 415; Conservative 50; Mismatches 69; Indels 6; Gaps 3;

```
OY 5 OEEFKLAGRALGKHLRLLEKROEGAEITLISADGPVTTQTRDPVVDCTCGFLPRRYI 64
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 18 KEGVANAAGDSIGILQKRLDGTNEGDAIELSEBRPVQTSARAPVDCSCCGIPKRII 77
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 65 IAIMSGLGFCISFGIRCNLGVAVISVMNNSTTHRGHVAVVQAKQSPDETYGLIHGSPF 124
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 78 IAVMSGLGFCISFGIRCNLGVAVIVEMNNSTYVQKPEIQTAQFNMPDETYGLIHGSPF 137
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 125 WGIYVTOIPGGFTICQKPAANRVFGAIVATSTLNMIPSAARVHGCIVFVRILOGLVHG 184
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 138 WGIYVTOIPGGFTISNKPFAANRVFGAIVATSTLNMIPSAARVHGCIVFVRILOGLVHG 197
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 185 VTPYPAHGIMSKWAPLERSRLATTAFGGSYAGAVVAMPAGLVLYOYSGMSSVFYVYGSF 244
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 198 VTPYPAHGIMSKWAPLERSRLATTAFGGSYAGAVVAMPAGLVLYOYSGMSSVFYVYGSF 257
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 245 GTFWTLFWLIVSYESPALHPISISEBRKYIEDAIGESAKLNPITKFTSPMRFFTSMPV 304
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 256 GIWMFMFLQAYECGAVHPTISNEERTYIETISIGGANLAS-LSKFTPMWRFFTSLPV 316
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 305 VAIIVANPCRSWTFYLLISQPDYFEVFGFEISKVGLVSALPHLVMTIIVPIGQIADF 364
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 317 VAIIVANPCRSWTFYLLISQPAYFEVFGFAISKVGLLSAVPHVMWMTIIVPIGQIADY 376
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 365 LRSRRIMSTTVNRKILMNCGFGMEATLLLVGYSHSKGVAISFLVAVGFSGFAISGFNV 424
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 377 LRSRILITTTAVARKILMNCGFGMEATLLLVGFSHTKGVAISFLVAVGFSGFAISGFNV 436
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 425 NMLDIAPRASILMISNGVGLTSGMVCPIVGMATKTKTREEMQVYFLIALVHYSGVI 484
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 437 NMLDIAPRASILMISNGVGLTSGMVCPLIVGAMTKTKTREEMQVYFLIALVHYSGVI 496
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
OY 485 FYGVASGEKQWAPBEEMSEKCGFVGHDLAAGSDSDSEMEDBAPPGAPAPPPSYGAT 544
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 497 FYGVASGEKQWAPBEEMSEKCGIITDDELA--EETELNHEA--FVSPKKMSYGAT 551
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

RESULT 13

```
OYNDX2 PRELIMINARY; PRT; 589 AA.
AC OYNDX2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Vesicular glutamate transporter 3.
GN Name=VGLUT3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=22146126; PubMed=12151341; DOI=10.1093/embo-reports/kvfi59;
RA Takamori S., Malherbe P., Broger C., Jahn R.;
RT "Molecular cloning and functional characterization of human vesicular
RT glutamate transporter 3 ";
RL EMBL Rep. 3:798-803(2002).
DR EMBL; AJ459241; CAD30553.1; -.
DR Genew; HGNC:20151; SLC17A8.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00850; MFS; 1.
SQ SEQUENCE 589 AA; 64991 MW; E74DDC91495F8775 CRC64;
```

Query Match 73.6%; Score 2185; DB 2; Length 589;
Best Local Similarity 76.3%; Pred. No. 6.4e-156;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

```
QY 5 QEBRKLGRALGKLRLEKROGAEETLEISADGRPYTQTRDPVVDCTCFGLPRRYI 64
D 18 KEGVKNAGVDSGLGIRKIDGTDEEDNIELEBERPVQTSRPSPLDCHCCGPKRYI 77
QY 65 IAINSGIGFCISFGIRCNLGAIVSMVNNSTTHRGVAVVQKAPSWDPETVGLIHGSPF 124
D 78 IAINSGIGFCISFGIRCNLGAIVSMVNNSTTHRGVAVVQKAPSWDPETVGLIHGSPF 137
QY 125 MGVIIVTQIRGFIQOKFPAANVFPGAIVATSTLNLISAAVHYGCIYFRILQGLVEG 184
D 138 MGVIIVTQIRGFIQOKFPAANVFPGAIVATSTLNLISAAVHYGCIYFRILQGLVEG 197
QY 185 VTYPACGIGNSKMAPLERSRLATTAFCGSYAGAVVAMPGLGVLYQVSGMSVFPVYGSF 244
D 198 VTYPACGIGNSKMAPLERSRLATTAFCGSYAGAVVAMPGLGVLYQVSGMSVFPVYGSF 257
QY 245 GIPWYLFVWLVSYSPALHPSISEBERKYIDATGESAKLNNPLTKFSTPMRPFSTMPV 304
D 258 GIIVYMFVWLVSYSPALHPSISEBERKYIDATGESAKLNNPLTKFSTPMRPFSTMPV 316
QY 305 YAIIVANFCRSWTYLLISQPDYFEEVFGFESIKVGLVSLPHLVMTIIVPIGQINDF 364
D 317 YAIIVANFCRSWTYLLISQPDYFEEVFGFESIKVGLVSLPHLVMTIIVPIGQINDF 376
QY 365 LRSBRIMSTNVKRLMNCGFGMEATLLVVGYSKGVASISPLVAVGSGFAISGFNV 424
D 377 LRSBRIMSTNVKRLMNCGFGMEATLLVVGYSKGVASISPLVAVGSGFAISGFNV 436
QY 425 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVYELISLVHYGVI 484
D 437 NHDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVYELISLVHYGVI 496
QY 485 FYGVFASGEKOPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPPGAPPAPEPSYCAT 544
D 497 FYGVFASGEKOPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPPGAPPAPEPSYCAT 551

RESULT 14
Q8BF08 PRELIMINARY; PRT; 601 AA.
ID Q8BF08
AC Q8BF08
DT 01-MAR-2003 (Tremblrel. 23. Created)
DT 01-MAR-2003 (Tremblrel. 23. Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28. Last annotation update)
DS Vesicular glutamate transporter-3.
GN Name=Slc17a8; Synonyms=Vglut3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Sculter G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Steadton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Bock S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wiley J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
```

```
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Director MGC Project;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=whole brain;
RX PubMed=12384506; DOI=10.1074/jbc.M206739200;
RA Schaefer M.K., Varoqui H., Defamie N., Weihe E., Erickson J.D.;
RT "Molecular cloning and functional identification of mouse vesicular
RT glutamate transporter 3 and its expression in subsets of novel
RT excitatory neurons."
RL J. Biol. Chem. 277:50734-50748 (2002).
DR EMBL; BC042593; AA042593.1; -.
DR EMBL; AF510321; AAN74643.1; -.
DR MGD; MGI:303629; Slc17a8.
DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR GO; GO:0005113; F:L-glutamate transporter activity; IDA.
DR GO; GO:0015813; F:L-glutamate transporter; IDA.
DR InterPro; IPR003006; IPR_003006.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00850; MFS; 1.
SQ SEQUENCE 601 AA; 66148 MW; B6F6C6E0C64961B CRC64;

Query Match 72.5%; Score 2154.5; DB 2; Length 601;
Best Local Similarity 74.0%; Pred. No. 1.3e-153;
Matches 409; Conservative 53; Mismatches 72; Indels 19; Gaps 4;

QY 5 QEBRKLGRALGKLRLEKROGAEETLEISADGRPYTQTRDPVVDCTCFGLPRRYI 64
D 18 KEGVKNAGVDSGLGIRKIDGTDEEDNIELEBERPVQTSRPSPLDCHCCGPKRYI 77
QY 52 VDCFCGPRRYIYAINSGIGFCISFGIRCNLGAIVSMVNNSTTHRGVAVVQKAPSW 111
D 78 CDCSCGPKRYIYAINSGIGFCISFGIRCNLGAIVSMVNNSTTHRGVAVVQKAPSW 137
QY 112 DPEIVGLIHGSPFNGVITVQIRGFIQOKFPAANVFPGAIVATSTLNLISAAVHYG 171
D 138 DPEIVGLIHGSPFNGVITVQIRGFIQOKFPAANVFPGAIVATSTLNLISAAVHYG 197
QY 172 VIFVRIIQLGVEGYTPACGIGNSKMAPLERSRLATTAFCGSYAGAVVAMPGLGVLYQ 231
D 198 VIFVRIIQLGVEGYTPACGIGNSKMAPLERSRLATTAFCGSYAGAVVAMPGLGVLYQ 257
QY 232 SGMSVFPVYVGSFGIPWYLFVWLVSYSPALHPSISEBERKYIDATGESAKLNNPLTKF 291
D 258 IGMASVFPVYVGSFGIPWYLFVWLVSYSPALHPSISEBERKYIDATGESAKLNNPLTKF 316
QY 292 STPMRPFSTMPVYAIIVANFCRSWTYLLISQPDYFEEVFGFESIKVGLVSLPHLV 351
D 317 NTMRRPFSTMPVYAIIVANFCRSWTYLLISQPDYFEEVFGFESIKVGLVSLPHLV 376
QY 352 TIIVPIGQINDFRLSRIMSTNVKRLMNCGFGMEATLLVVGYSKGVASISPLVLA 411
D 377 TIIVPIGQINDFRLSRIMSTNVKRLMNCGFGMEATLLVVGYSKGVASISPLVLA 436
QY 412 VGFSGPAGISGNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQV 471
D 437 VGFSGPAGISGNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQV 496
QY 472 FLIASLVHYGVIYGVFASGEKOPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPP 531
D 497 FLIASLVHYGVIYGVFASGEKOPMABPEEMSEKCGFVGHDLQAGSDSEMEDAEPP 551
QY 532 GAPPAPPEPSYCAT 544
D 552 FVSPRKTMSYCAT 564
```

RESULT 15
Q7TOH3 PRELIMINARY; PRT; 402 AA.
ID 07TOH3;
AC 07TOH3;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Solute carrier family 17 (Sodium-dependent inorganic phosphate
cotransporter), member 7.
GN Name=Slc17a7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stepleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uebli T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Director MGC Project;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054462; AAH54462.1; -;
DR GO; GO:0042137; P:neurotransmitter storage; IMP.
DR InterPro; IPR007114; MFS.
DR PROSITE; PSS0850; MFS; 1.
SQ SEQUENCE 402 AA; 44140 MW; 62844306CB033DD0 CRC64;
Query Match 70.9%; Score 2107; DB 2; Length 402;
Best Local Similarity 98.5%; Pred. No. 3e-150;
Matches 396; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 159 MLPSARHYHGVFVRLLOGIVEGVTPACHGIMSKWAPPLERSRLTTFACGSYAGA 218
DB 1 MLPSARHYHGVFVRLLOGIVEGVTPACHGIMSKWAPPLERSRLTTFACGSYAGA 60
QY 219 VVAMPPLAGLVQYSGMSVFYVYGSFGIFMYLFWLLVSESPALHPSISEERKYTEDAI 278
DB 61 VVAMPPLAGLVQYSGMSVFYVYGSFGIFMYLFWLLVSESPALHPSISEERKYTEDAI 120
QY 279 GESAKLMNPLTFESTPMRRFPTSMRYAIIIVANFCRSWTFYLLISQPDYFEEVFGFEIS 338
DB 121 GESAKLMNPLTFESTPMRRFPTSMRYAIIIVANFCRSWTFYLLISQPDYFEEVFGFEIS 180
QY 339 KVGIVSALPHLVMTIIVPIGGQIADFLRSRRINSTTNVAKLMNCGFGMEATLLLVGYS 398
DB 181 KVGIVSALPHLVMTIIVPIGGQIADFLRSRRINSTTNVAKLMNCGFGMEATLLLVGYS 240
QY 399 HSKGVAISFLVAVGSGFPAISGFNNHDIAPRYASILMGISNGVGLTSGMVCPTIVGA 458
DB 241 HSKGVAISFLVAVGSGFPAISGFNNHDIAPRYASILMGISNGVGLTSGMVCPTIVGA 300

QY 459 MTKHKTREEMQYVPLIASIVHYGVIFGVFASGEKOPWAEPEEMSEKCGFVGHDLAG 518
DB 301 MTKHKTREEMQYVPLIASIVHYGVIFGVFASGEKOPWAEPEEMSEKCGFVGHDLAG 360
QY 519 SDDSEMEDAEPPGAPPAAPPSPYGAHSTFPQPPRPAPPVVDY 560
DB 361 SDDSEMEDAEPPGAPPAAPPSPYGAHSTFPQPPRPAPPVVDY 402

Search completed: June 2, 2005, 11:31:39
Job time : 182 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:17:01 ; Search time 163 Seconds
(without alignments)
1328.747 Million cell updates/sec

Title: US-10-734-731-4
Perfect score: 2970
Sequence: 1 MEFRQEFRLAGRALGKHL.....YGATHSTFPQPPPPYRDY 560

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001s:*
5: geneseq2002s:*
6: geneseq2003as:*
7: geneseq2003bs:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2970	100.0	560	2 AAW05148	AAW05148 Human bra
2	2970	100.0	560	6 ABG74792	ABG74792 Human BNP
3	2970	100.0	560	7 ADCl15484	ADCl15484 Human BNP
4	2967	99.9	560	2 AAW70500	AAW70500 Human sod
5	2962	99.7	560	6 ABG74791	ABG74791 Human BNP
6	2962	99.7	560	7 ADCl15482	ADCl15482 Human BNP
7	2962	99.7	560	4 ADD01474	ADD01474 Human VGL
8	2962	99.7	567	4 AAO13870	AAO13870 Human pol
9	2929	98.6	560	6 ABG74794	ABG74794 Murine BN
10	2929	98.6	560	7 ADCl15488	ADCl15488 Mouse BNP
11	2925	98.5	560	6 ABG74793	ABG74793 Rat BNP1
12	2925	98.5	560	6 ADCl15486	ADCl15486 Rat BNP1
13	2317.5	78.0	582	6 ABG74795	ABG74795 Human DNP
14	2317.5	78.0	582	7 ADCl15490	ADCl15490 Human DNP
15	2317.5	78.0	582	7 ADD01475	ADD01475 Human VGL
16	2313.5	77.9	578	7 ADG88331	ADG88331 Rat trans
17	2313.5	77.9	582	6 ABG74796	ABG74796 Rat DNP1
18	2313.5	77.9	582	6 ABG74797	ABG74797 Murine DN
19	2313.5	77.9	582	6 ABM04787	ABM04787 Rat Na-de
20	2313.5	77.9	582	7 ADCl15494	ADCl15494 Mouse DNP
21	2313.5	77.9	582	7 ADCl15492	ADCl15492 Rat DNP1
22	2307.5	77.7	582	4 AAW79273	AAW79273 Human pro
23	2185	73.6	589	5 AAU99329	AAU99329 Human tra
24	2185	73.6	589	6 AAO30994	AAO30994 Human tra
25	2185	73.6	589	7 ADD01392	ADD01392 Human TCH

26	2185	73.6	589	7 ADG88329	ADG88329 Human tra
27	2185	73.6	589	8 ADR10021	ADR10021 Human pro
28	2174.5	73.2	860	5 ABB07689	ABB07689 Rat gluta
29	2154.5	72.5	601	7 ADD01410	ADD01410 Mouse TCH
30	2138.5	72.0	566	7 ADJ95072	ADJ95072 Novel NOV
31	1980.5	66.7	588	6 AAE32079	AAE32079 Human TRI
32	1297	43.7	576	2 AAW88523	AAW88523 Eat-4 pro
33	1297	43.7	576	8 ADN23170	ADN23170 Bacterial
34	1198.5	40.4	560	4 ABB59401	ABB59401 Drosophil
35	1186	39.9	264	7 ADM04596	ADM04596 Human pro
36	1025.5	34.5	204	7 ADB64099	ADB64099 Human pro
37	986.5	33.2	502	4 ABB65873	ABB65873 Drosophil
38	986.5	33.2	573	8 ABB60525	ABB60525 Drosophil
39	971	32.7	573	8 ADN23219	ADN23219 Bacterial
40	971	32.7	573	8 ADN23218	ADN23218 Bacterial
41	950	32.0	544	8 ADN23220	ADN23220 Bacterial
42	940	31.6	495	3 AA45087	AA45087 Partial h
43	940	31.6	495	4 AAB66967	AAB66967 Human AST
44	940	31.6	495	8 ADJ75516	ADJ75516 Marker ge
45	940	31.6	495	8 ADR14587	ADR14587 Human NF-

ALIGNMENTS

RESULT 1
AAW05148 standard; protein; 560 AA.
ID AAW05148;
AC AAW05148;
AD 30-JAN-1997 (first entry)
DE Human brain sodium-dependent inorganic phosphate cotransporter.
DS Brain sodium-dependent inorganic phosphate cotransporter; hBNP1.
KW Homo sapiens.
OS
XX
XX W09634288-A1.
XX PD 31-OCT-1996.
XX PF 25-APR-1996; 96WC-US005792.
XX PR 27-APR-1995; 95US-00430033.
XX PA (BL1L) LILLY & CO ELI.
XX NI B, Paul SM;
XX WPI; 1996-497773/49.
XX DR N-PSDB; AAT42064.
XX PT New isolated human brain sodium-dependent inorganic phosphate co-
PT transporter - used to develop probe for diagnosis, treatment and
PT prevention of conditions involving inappropriate stimulation.
XX PS Claim 1; Page 55-57; 68pp; English.
XX A novel human brain sodium-dependent inorganic phosphate cotransporter
XX (AAW05148), designated hBNP1, is selectively expressed in discrete
XX populations of neurons and glia. Its amino acid sequence was deduced from
XX a cDNA clone (AAT42064) isolated from a human hippocampus cDNA library.
XX hBNP1 can be expressed in transformed host cells and used to determine
XX the effectiveness of test cpds. for the treatment or prevention of
XX disorders associated with an inappropriate stimulation of hBNP1
SQ Sequence 560 AA;
Query Match 100.0%; Score 2970; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 5.2e-267;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MEFROEERKLAGRALGKHLRLLEKROGAETLELSADGRPVYTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKHLRLLEKROGAETLELSADGRPVYTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSSTHRCGHVVOGAQFSMDPETVGLIH 120
DB 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSSTHRCGHVVOGAQFSMDPETVGLIH 120
QY 121 GSFHWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFPRILQG 180
DB 121 GSFHWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFPRILQG 180
QY 181 LVEGVTPACGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFPY 240
DB 181 LVEGVTPACGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFPY 240
QY 241 YGSFGIFWYLFWLVSYESPALHPSISEERKXIEDALGESAKLMNPLTKFSTPMRRPFT 300
DB 241 YGSFGIFWYLFWLVSYESPALHPSISEERKXIEDALGESAKLMNPLTKFSTPMRRPFT 300
QY 301 SMPVVAIIIVANFCRSWTFYLLISODPYEEVFGFEBISKVLVSALPHLWMTIIVPIGQ 360
DB 301 SMPVVAIIIVANFCRSWTFYLLISODPYEEVFGFEBISKVLVSALPHLWMTIIVPIGQ 360
QY 361 IADFLRSRRIIMSTNVKRLMNCGFGMEATLLVVGYSKGVASFLVLA VFGSGFALS 420
DB 361 IADFLRSRRIIMSTNVKRLMNCGFGMEATLLVVGYSKGVASFLVLA VFGSGFALS 420
QY 421 GENVNHLDIAPRYASILNGISNGVTLSGMVCPIIVGAMTKTKTEEMQYVFLIASLVHY 480
DB 421 GENVNHLDIAPRYASILNGISNGVTLSGMVCPIIVGAMTKTKTEEMQYVFLIASLVHY 480
QY 481 GGVITYGVFASGEKOPMAPEPEMSEKCGFVGHDLAGSDSEMEDAEAPPAAPPAPS 540
DB 481 GGVITYGVFASGEKOPMAPEPEMSEKCGFVGHDLAGSDSEMEDAEAPPAAPPAPS 540
QY 541 YGATHSTFOPPRPPPPVVDY 560
DB 541 YGATHSTFOPPRPPPPVVDY 560

RESULT 2
ABG74792
ID ABG74792 standard; protein; 560 AA.
AC ABG74792;
DT 10-JUN-2003 (first entry)
DE Human BNPI protein #2.
XX BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;
XX pain-regulation; glutamate transport mediator; musculo-skeletal pain;
XX brain sodium-dependent inorganic phosphate cotransporter; analgesic;
XX brain inorganic phosphate cotransporter; antimigraine; chronic pain;
XX differentiation-associated sodium-dependent inorganic phosphate
XX cotransporter; neuronal; mechanical hyperalgesia; diabetic neuropathy;
XX visceral pain; cerebral pain; peripheral pain; inflammatory pain;
XX cluster headache; trigeminal neuralgia; enzyme.
XX Homo sapiens.
XX OS
XX PN MO2002101394-A2.
XX
XX PD 19-DEC-2002.
XX
XX PF 13-JUN-2002; 2002WO-EP006484.
XX
XX PR 13-JUN-2001; 2001DB-01028541.
XX
XX PA (CHEF ) GRUENENTHAL GMBH.
XX
```

```
PI Weihe E, Schaefer MK;
XX
XX MPI: 2003-148635/14.
DR N-PSDB; ABX13550.
XX
XX PT Identifying pain-regulating compounds, useful particularly for treating
PT chronic pain, based on interaction with specific phosphate
XX cotransporters.
XX
XX PS Claim 1a; Fig 1d; 104pp; German.
XX
XX CC This invention describes a novel method for identifying pain-regulating
CC substances. The method comprises incubating a test substance with BNPI
CC (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC (differentiation-associated sodium-dependent inorganic phosphate
CC cotransporter then measuring either binding of the test substance to BNPI
CC or DNPI or some functional property of the proteins that is altered by
CC binding to the test substance. The novel pain-regulating substances have
CC analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC glutamate transport. The products of the invention are used for treating
CC chronic pain, particularly musculo-skeletal, neuropathic (especially
CC allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC cluster headache and trigeminal neuralgia. This sequence represents the
CC human BNPI polypeptide encoded by a polynucleotide (deposited in
CC AAT420649) which is used in the method disclosed in the invention
XX
XX SQ Sequence 560 AA;
XX
XX Query Match 100.0%; Score 2970; DB 6; Length 560;
XX Best Local Similarity 100.0%; Pred. No. 5.2e-267;
XX Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MEFROEERKLAGRALGKHLRLLEKROGAETLELSADGRPVYTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKHLRLLEKROGAETLELSADGRPVYTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSSTHRCGHVVOGAQFSMDPETVGLIH 120
DB 61 RRYIIAIMGSLGFCISFGIRCNLGVAIIVSMVNSSTHRCGHVVOGAQFSMDPETVGLIH 120
QY 121 GSFHWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFPRILQG 180
DB 121 GSFHWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFPRILQG 180
QY 181 LVEGVTPACGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFPY 240
DB 181 LVEGVTPACGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFPY 240
QY 241 YGSFGIFWYLFWLVSYESPALHPSISEERKXIEDALGESAKLMNPLTKFSTPMRRPFT 300
DB 241 YGSFGIFWYLFWLVSYESPALHPSISEERKXIEDALGESAKLMNPLTKFSTPMRRPFT 300
QY 301 SMPVVAIIIVANFCRSWTFYLLISODPYEEVFGFEBISKVLVSALPHLWMTIIVPIGQ 360
DB 301 SMPVVAIIIVANFCRSWTFYLLISODPYEEVFGFEBISKVLVSALPHLWMTIIVPIGQ 360
QY 361 IADFLRSRRIIMSTNVKRLMNCGFGMEATLLVVGYSKGVASFLVLA VFGSGFALS 420
DB 361 IADFLRSRRIIMSTNVKRLMNCGFGMEATLLVVGYSKGVASFLVLA VFGSGFALS 420
QY 421 GENVNHLDIAPRYASILNGISNGVTLSGMVCPIIVGAMTKTKTEEMQYVFLIASLVHY 480
DB 421 GENVNHLDIAPRYASILNGISNGVTLSGMVCPIIVGAMTKTKTEEMQYVFLIASLVHY 480
QY 481 GGVITYGVFASGEKOPMAPEPEMSEKCGFVGHDLAGSDSEMEDAEAPPAAPPAPS 540
DB 481 GGVITYGVFASGEKOPMAPEPEMSEKCGFVGHDLAGSDSEMEDAEAPPAAPPAPS 540
QY 541 YGATHSTFOPPRPPPPVVDY 560
DB 541 YGATHSTFOPPRPPPPVVDY 560
```


RESULT 3
ADCL15484
ID ADCL15484 standard; protein; 560 AA.
AC
XX ADCL15484;
XX
DT 18-DEC-2003 (first entry)
DE
XX Human BNPI protein #2.
BNPI: DNP1;
brain-associated sodium-dependent inorganic phosphate transporter;
differentiation-associated inorganic phosphate transporter;
ophthalmological; auditory; neuroleptic; antimanic; antidepressant;
cerebroprotective; neuroprotective; analgesic; anorectic; anticoagulant
antiparkinsonian; vasotropic; antiemetic; antiarthritic; tranquilizer;
vincidic; antibacterial; procoagulant; antiinflammatory; cardiact;
hypotensive; antiaesthetic; immunosuppressive; antidiabetic;
antialcolic; anti-HIV; nootropic; antiallergic; gene therapy;
vision disorder; retinitis pigmentosa; optical degeneration;
hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
depression; stroke; brain trauma; paralysis;
amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
anorexia nervosa; epilepsy; hemibalism; Huntington chorea; stress;
Parkinson's disease; cataract; arthritis; hyperactivity;
developmental disorder; rabies; infection; influenza; malaria; CJD;
inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis
asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
autonomic disorder; digestive tract disorder; nervous system disorder;
neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
piron disease; demyelination; multiple sclerosis; retinal degeneration
glaucoma; myasthenia; retinal detachment; ataxia; memory disorder;
cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
sleep disorder; neurocoxicological disease; spinal motor neuron disease;
muscular atrophy; neuroinflammation; fever; taste disorder; food allergy
aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
neuroprotectoin; enzyme.
XX Homo sapiens.
XX MO2003029828-A2.
XX
PN 10-APR-2003.
PD
XX
PF 24-SEP-2002; 2002MO-EP010707.
XX
PR 24-SEP-2001; 2001DE-01047006.
PR 25-SEP-2001; 2001DE-01047028.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
XX Weihe E, Schaefer MK;
XX
XX WPI, 2003-354751/33.
DR N-PSDB; ADCL15483.
XX
PT Identifying agents for treatment and diagnosis of diseases, e.g.
PT depression or viral infections, from binding to inorganic phosphate
PT transporters, also new agents.
XX
PS Claim 1, Fig 1d, 129pp; German.
XX
CC This invention describes a novel method of identifying agents for
CC detection or treatment of specified conditions. The method comprises
CC incubating test compound with BNPI or DNP1 (brain or differentiation-
CC associated sodium-dependent inorganic phosphate transporter), or related
CC proteins, nucleic acids or cells (and/or cell preparations), then
CC measuring binding of test compound or some functional parameter altered
CC by binding. The products of the invention have ophthalmological,
CC auditory, neuroleptic, antimanic, antidepressant, cerebroprotective,

CC	neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
CC	vasotrophic, antiemetic, antianthritic, tranquilizer, vitrucide,
CC	antibacterial, protozoacide, antiinflammatory, caditant, hypotensive,
CC	antiasmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
CC	nootropic and antiallergic activity. The method is used to identify
CC	agents for diagnosis and treatment (including gene therapy) of disorders
CC	of vision; retinitis pigmentosa; optical degeneration; hearing disorders
CC	or loss; timbuna; Meniere's disease; schizophrenia; mania; depression
CC	stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
CC	sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
CC	epilepsy; hemibalism; Huntington chorea; stress; Parkinson's disease;
CC	transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
CC	cateract; arthritis; hyperactivity; developmental disorders; rabies;
CC	bacterial and viral infections; influenza; malaria; CJD; inflammatory
CC	bowel disease; Crohn's disease; cardio-vascular and -respiratory
CC	functional disorders; hypertension; barorefferent and chemorefferent
CC	diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
CC	nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
CC	HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
CC	systems; overexcitability, particularly mediated by glutamate;
CC	neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
CC	bacterial, Rasmussen or HIV); prion diseases; demyelination
CC	(particularly multiple sclerosis); retinal degeneration; glaucoma;
CC	nyctagnus; retinal detachment; diseases of cerebellum (ataxia), basal
CC	ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
CC	learning and cognitive disorders; stiff-man or restless leg syndromes;
CC	anxiety; phobia; sleep disorders; drug dependency, addiction or
CC	withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
CC	hepatoenkephalopathy, with or without alcohol intoxication;
CC	neurotoxicological diseases; spinal motor neuron diseases; muscular
CC	atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
CC	taste disorders; food allergies; Chinese restaurant syndrome; aggression;
CC	paranoia; tremors; neuroendocrine disorders; Tourette syndrome;
CC	cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
CC	burn-out syndrome; sudden infant death syndrome; cardiac infarct;
CC	insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
CC	dysfunction (impotence); priapism); also promotion of microglial activity,
CC	learning, cognition or memory; neuroprotection; diagnosis of neurostatic
CC	disease, and as adjuvant therapy for electrostimulation of the
CC	subthalamic nucleus in Parkinson's disease. This sequence represents a
CC	human BNP1 protein described in the disclosure of the invention.
CC	
XX	
SQ	Sequence 560 AA;
	Query Match 100.0%; Score 2970; DB 7; Length 560;
	Best Local Similarity 100.0%; Pred. No. 5.2e-267;
	Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MEFRQEBERKLAKGALGKHLRLKEKROGAEITLSADGRVTTQOTEDPPVADCTCEFLP 60
DB	1 MEFRQEBERKLAKGALGKHLRLKEKROGAEITLSADGRVTTQOTEDPPVADCTCEFLP 60
QY	61 RRYIIAMSGIGFCISFGIRCNLGVAIYVWNNSTTRHGSHVVQKAFSMDPEVTGLIH 120
DB	61 RRYIIAMSGIGFCISFGIRCNLGVAIYVWNNSTTRHGSHVVQKAFSMDPEVTGLIH 120
QY	121 GSFPMGTVLVQDIPGGFICQKPAARVGFALVAISTNMLIPSAARHYGCVIFVRLIQG 180
DB	121 GSFPMGTVLVQDIPGGFICQKPAARVGFALVAISTNMLIPSAARHYGCVIFVRLIQG 180
QY	181 LVEGTVYDACHGISMKNAPLERSRLLATTCGSGYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
DB	181 LVEGTVYDACHGISMKNAPLERSRLLATTCGSGYAGAVVAMPPLAGVLVOYSGMSSVFYV 240
QY	241 YGSGFIPIWYLEFWLLVSYESPALPHDSIEBEERYIEDAIGESAKIMNPLTKFSTPWRNFT 300
DB	241 YGSGFIPIWYLEFWLLVSYESPALPHDSIEBEERYIEDAIGESAKIMNPLTKFSTPWRNFT 300
QY	301 SMPVYAIIVANFCGSMFTFYLLISQDPYFEVVPFPELSKYGLVSLPHVWTTIIVPIGGQ 360
DB	301 SMPVYAIIVANFCGSMFTFYLLISQDPYFEVVPFPELSKYGLVSLPHVWTTIIVPIGGQ 360
QY	361 IADFLRSRRINSTNVRKLNMGCGFGMEATLLLVGSHSGKVAISFLVLAVGFSGFAIS 420

Db 361 IADFLRSRRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVALSFVLAVGSGFAIS 420
QY 421 GGNVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIYGAMTKHKTREMOYVFLIASLVHY 480
Db 421 GGNVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIYGAMTKHKTREMOYVFLIASLVHY 480
QY 481 GGVIIFYGVFASGEGKPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
Db 481 GGVIIFYGVFASGEGKPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATHSTFQPPRPPPPVVDY 560
Db 541 YGATHSTFQPPRPPPPVVDY 560

RESULT 4
AAW70500
ID AAW70500 standard; protein; 560 AA.

XX AAW70500;

DT 18-JAN-1999 (first entry)

DE Human sodium-lithium countertransporter BNPI.

KW Sodium-lithium countertransporter; sodium-phosphate cotransporter; BNPI;
human; lithium therapy; manic depression.

OS Homo sapiens.

PN WO9838203-A1.

PD 03-SEP-1998.

PF 11-FEB-1998; 98WO-US002875.

PR 27-FEB-1997; 97US-0039462P.

PA (UYEM-) UNIV EMORY.

PI Gunn RB, Timmer RT;

XX WPI; 1998-520759/44.

DR N-PSDB; AAV33503.

PT New isolated lithium-sodium counter-transporter DNA - used to develop
products for evaluating lithium-sodium transport in erythrocytes,
particularly for lithium therapy in manic depression.

PS Claim 8; Page 45-47; 64pp; English.

XX This polypeptide comprises the brain-specific human lithium-sodium
countertransporter (USCT) BNPI. A DNA sequence for human BNPI is provided
(see AAV33503). LSTs such as BNPI provide the physiological mechanism
for the extrusion of lithium from cells, i.e. it regulates the cell
concentration of lithium. Its activity determines the therapeutic effect
of lithium. The invention provides a simple molecular biological test for
the ability of cells to extrude lithium. The LSTs have significance for
determining the responsiveness of humans with mental disorders, including
CC manic depressives, to treatment with lithium salts. Probes and primers
for BNPI, P1T-1 (see AAW70498), P1T-2 (see AAW70499) can be used in
CC diagnostic tests useful for genetic screenings to predict whether a
CC patient will respond to lithium treatment. The test is also a screen for
CC susceptibility to, and extent of, manic depressive illness, and is
CC suitable for screening newborns

XX Sequence 560 AA;

Query Match 99.9%; Score 2967; DB 2; Length 560;
Best Local Similarity 99.8%; Pred. No. 9.9e-267;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFRQEBFRKLAGRALGKIHLEKROGAEETLEISADGRPTTQTRDPVVDCTCFGLP 60
Db 1 MEFRQEBFRKLAGRALGKIHLEKROGAEETLEISADGRPTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAINGSGFGFCISFGIRCNLGAIVSMVNNSTTHRGHVVVOKAQSPDETVGLIH 120
Db 61 RRYIIAINGSGFGFCISFGIRCNLGAIVSMVNNSTTHRGHVVVOKAQSPDETVGLIH 120
QY 121 GSFPMGYIVTQJPGFICQKFAANRVFGFAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
Db 121 GSFPMGYIVTQJPGFICQKFAANRVFGFAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
QY 181 IVEGYTPACGICWSKMAPPLERSRLATTAFCGSAAGAVAMPPLAGVLYQVSGMSVFYV 240
Db 181 IVEGYTPACGICWSKMAPPLERSRLATTAFCGSAAGAVAMPPLAGVLYQVSGMSVFYV 240
QY 241 YGSPGIFMWLFMWLVSYSPALHPISIEBERKIIDALGESAKLNNPLTKSTPMRRPFT 300
Db 241 YGSPGIFMWLFMWLVSYSPALHPISIEBERKIIDALGESAKLNNPLTKSTPMRRPFT 300
QY 301 SMPVYAIIVANFCRSMTFYLLISQPDYEEVFGFEISKVGLVSLPHLWMTIIVPIGQ 360
Db 301 SMPVYAIIVANFCRSMTFYLLISQPDYEEVFGFEISKVGLVSLPHLWMTIIVPIGQ 360
QY 361 IADFLRSRRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVALSFVLAVGSGFAIS 420
Db 361 IADFLRSRRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVALSFVLAVGSGFAIS 420
QY 421 GGNVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIYGAMTKHKTREMOYVFLIASLVHY 480
Db 421 GGNVNHLDIAPRYASIIIMGISNGVGLSGMVCPIIYGAMTKHKTREMOYVFLIASLVHY 480
QY 481 GGVIIFYGVFASGEGKPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
Db 481 GGVIIFYGVFASGEGKPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATHSTFQPPRPPPPVVDY 560
Db 541 YGATHSTFQPPRPPPPVVDY 560

RESULT 5
ABG74791
ID ABG74791 standard; protein; 560 AA.

XX ABG74791;

DT 10-JUN-2003 (first entry)

DE Human BNPI protein.

KW BNPI; sodium-dependent inorganic phosphate cotransporter; DNP1;
pain-regulation; glutamate transport mediator; musculo-skeletal pain;
brain sodium-dependent inorganic phosphate cotransporter; analgesic;
brain inorganic phosphate cotransporter; antimigraine; chronic pain;
differentiation-associated inorganic phosphate cotransporter; migraine;
neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
visceral pain; cerebral pain; peripheral pain; inflammatory pain;
cluster headache; trigeminal neuralgia; P1M-1 kinase; enzyme.

OS Homo sapiens.

PN WO2002101394-A2.

PD 19-DEC-2002.

PF 13-JUN-2002; 2002WO-EP006484.

PR 13-JUN-2001; 2001DE-01028541.

PA (CHEP) GRUENENTHAL GMBH.

PI Weihe E, Schaefer WK;

XX WPI; 2003-148835/14.
DR N-PSDB; ABX13549.
XX
XX Identifying pain-regulating compounds, useful particularly for treating
PT chronic pain, based on interaction with specific phosphate
PT cotransporters.
XX
XX Claim 1a; Fig 1b; 104pp; German.
XX
XX This invention describes a novel method for identifying pain-regulating
CC substances. The method comprises incubating a test substance with BNPI
CC (brain sodium-dependent inorganic phosphate cotransporter) or DNPI
CC (differentiation-associated sodium-dependent inorganic phosphate
CC cotransporter) then measuring either binding of the test substance to BNPI
CC or DNPI or some functional property of the proteins that is altered by
CC binding to the test substance. The novel pain-regulating substances have
CC analgesic and antimigraine activity. BNPI and DNPI are mediators of
CC glutamate transport. The products of the invention are used for treating
CC chronic pain, particularly musculo-skeletal, neuropathic (especially
CC allodynic pain, mechanical hyperalgesia or diabetic neuropathy),
CC visceral, cerebral, peripheral and/or inflammatory pain, also migraine,
CC cluster headache and trigeminal neuralgia. This sequence represents the
CC human BNPI polypeptide (also described as P1W-1 kinase) encoded by a
CC polynucleotide deposited in NM_020309 which is used in the method
CC disclosed in the invention
XX
XX Sequence 560 AA;

Query Match 99.7%; Score 2962; DB 6; Length 560;
Best Local Similarity 99.8%; Pred. No. 2.9e-266;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFOEERKAKAGALGKHLERKOGARTLELSANRVTYOTRPPVDDCTCFGLP 60
DB 1 MEFOEERKAKAGALGKHLERKOGARTLELSANRVTYOTRPPVDDCTCFGLP 60
QY 61 RRYIAIAMSGLGFCISFGIRCNLGAVALSYMNNSTTHRGHVVOKQFSDPETHGLH 120
DB 61 RRYIAIAMSGLGFCISFGIRCNLGAVALSYMNNSTTHRGHVVOKQFSDPETHGLH 120
QY 121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLPSARVHYGVIFVRILOG 180
DB 121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLPSARVHYGVIFVRILOG 180
QY 121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLPSARVHYGVIFVRILOG 180
DB 121 GSFFWGYIVTQIPGGFICQKFAANRVGFAIVATSTLMLPSARVHYGVIFVRILOG 180
QY 181 LVEGVTPACGIMSKAPPLERSRLATTAFCGYAGAVVAMPAGVIVQYSGMSVFFV 240
DB 181 LVEGVTPACGIMSKAPPLERSRLATTAFCGYAGAVVAMPAGVIVQYSGMSVFFV 240
QY 241 YGSGFIFWYLFWLVSYESPALHPSISEEERKYTEDAIGESAKIMNPLTKSTWRRPFT 300
DB 241 YGSGFIFWYLFWLVSYESPALHPSISEEERKYTEDAIGESAKIMNPLTKSTWRRPFT 300
QY 301 SMPVYAIIVANFCRSMWTFYLLISQPDYFEEVFGFELSKVGLVSLPHTLVTIIVPIGQ 360
DB 301 SMPVYAIIVANFCRSMWTFYLLISQPDYFEEVFGFELSKVGLVSLPHTLVTIIVPIGQ 360
QY 361 IADFLRRRIMSTNVKLNKCGFGMEATLLVVGISHKGVAILSPVLAVFGSGPAIS 420
DB 361 IADFLRRRIMSTNVKLNKCGFGMEATLLVVGISHKGVAILSPVLAVFGSGPAIS 420
QY 421 GFNVNHLDIAPRYASIMGINSNGVTLSCWVCPITIVGAMTGHKREEMQVFLASIVHY 480
DB 421 GFNVNHLDIAPRYASIMGINSNGVTLSCWVCPITIVGAMTGHKREEMQVFLASIVHY 480
QY 481 GGVIIFYGVAFSGEKOPWAEPEMESEKCGFVGHQDLAGSDSEMEDAEPPGAPAPPPS 540
DB 481 GGVIIFYGVAFSGEKOPWAEPEMESEKCGFVGHQDLAGSDSEMEDAEPPGAPAPPPS 540
QY 541 YGATHSTFOPPRRPPPPVADY 560
DB 541 YGATHSTFOPPRRPPPPVADY 560

RESULT 6
ID ADCl5482 standard; protein, 560 AA.
XX ADCl5482
XX AC ADCl5482;
XX 18-DEC-2003 (first entry)
XX DE Human BNPI protein #1.
XX
XX BNPI; DNPI;
XX brain-associated sodium-dependent inorganic phosphate transporter;
XX differentiation-associated inorganic phosphate transporter;
XX ophthalmological, auditory, neuroleptic, antianemic, antidepressant;
XX cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;
XX vitruclide; antibacterial; protozoacide; antiinflammatory; cardiant;
XX hypotensive; antiaslatic; immunosuppressive; antidiabetic;
XX antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;
XX vision disorder; retinitis pigmentosa; optical degeneration;
XX hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;
XX depression; stroke; brain trauma; paralysis;
XX amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;
XX anorexia nervosa; epilepsy; hemiparesis; Huntington chorea; stress;
XX Parkinson's disease; cataract; arthritis; hyperactivity;
XX developmental disorder; rabies; infection; influenza; malaria; CJD;
XX inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
XX asthma; autoimmune; neuropathy; diabetes; HIV; AIDS;
XX autonomic disorder; digestive tract disorder; nervous system disorder;
XX neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
XX prion disease; demyelination; multiple sclerosis; retinal degeneration;
XX glaucoma; myasthenia; retinal detachment; ataxia; memory disorder;
XX cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
XX sleep disorder; neurotoxicological disease; spinal motor neuron disease;
XX muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
XX aggression; paranoia; neuroendocrine disorder; Tourette syndrome;
XX sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
XX multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
XX neuroprotection; enzyme.
XX
XX Homo sapiens.
XX
XX WO2003029828-A2.
XX
XX 10-APR-2003.
XX
XX 24-SEP-2002; 2002WO-EP010707.
XX
XX 24-SEP-2001; 2001DE-01047006.
XX 25-SEP-2001; 2001DE-01047028.
XX
XX (CHEF) GRUBENTHAL GMBH.
XX
XX Wehe E, Schaefer MK;
XX
XX WPI; 2003-354751/33.
XX
XX Identifying agents for treatment and diagnosis of diseases, e.g.
PT depression or viral infections, from binding to inorganic phosphate
PT transporters, also new agents.
XX
XX Claim 1; Fig 1b; 129pp; German.
XX
XX This invention describes a novel method of identifying agents for
CC detection or treatment of specified conditions. The method comprises
CC incubating test compound with BNPI or DNPI (brain or differentiation-
CC associated sodium-dependent inorganic phosphate transporter), or related
CC proteins, nucleic acids or cells (and/or cell preparations), then
CC measuring binding of test compound or some functional parameter altered
CC by binding. The products of the invention have ophthalmological,
CC auditory, neuroleptic, antianemic, antidepressant, cerebroprotective,
CC neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,

CC vasotropic, antiemetic, antiarthritic, tranquilizer, virucide,
 CC antibacterial, protozoacide, antiinflammatory, cardiant, hypotensive,
 CC antiasthmatic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
 CC neurotropic and antiallergic activity. The method is used to identify
 CC agents for diagnosis and treatment (including gene therapy) of disorders
 CC of vision; retinitis pigmentosa; optical degeneration; hearing disorders
 CC or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
 CC stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
 CC sclerosis; neuropatia; weight regulation; obesity; anorexia nervosa;
 CC epilepsies; hemiballism; Huntington chorea; stress; Parkinson's disease;
 CC transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
 CC cataract; arthritis; hyperactivity; developmental disorders; rabies;
 CC bacterial and viral infections; influenza; malaria; CUD; inflammatory
 CC bowel disease; Crohn's disease; cardio-vascular and -respiratory
 CC functional disorders; hypertension; baroafferent and chemoafferent
 CC diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
 CC nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
 CC HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
 CC systems; overexcitability, particularly mediated by glutamate;
 CC neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
 CC bacterial, Rasmussen or HIV); prion diseases; demyelination
 CC (particularly multiple sclerosis); retinal degeneration; glaucoma;
 CC nyctalgia; retinal detachment; diseases of cerebellum (ataxia); basal
 CC ganglia; pallidum; hearing or balancing organs; auditory canal; memory;
 CC learning and cognitive disorders; stiff-man or restless leg syndromes;
 CC anxiety; phobia; sleep disorders; drug dependency, addiction or
 CC withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
 CC hepatocellularopathy; with or without alcohol intoxication;
 CC neurotoxicological diseases; spinal motor neuron diseases; muscular
 CC atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
 CC taste disorders; food allergies; Chinese restaurant syndrome; aggression;
 CC parosmia; tremors; neuroendocrine disorders; Tourette syndrome;
 CC cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
 CC burn-out syndrome; sudden infant death syndrome; cardiac infarct;
 CC insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
 CC dysfunction (impotence; priapism); also promotion of microglial activity,
 CC learning, cognition or memory; neuroprotection; diagnosis of neurostatic
 CC disease, and as adjuvant therapy for electrostimulation of the
 CC subthalamic nucleus in Parkinson's disease. This sequence represents the
 CC human BMP1 protein also represented in AN: NM_020309.

XX Sequence 560 AA;

Query Match 99.7%; Score 2962; DB 7; Length 560;
 Best Local Similarity 99.8%; Pred. No. 2.9e-266;
 Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFROEERFKLAGRAIGKHLRLKROGAEETELSLADGRPTTQTRDDPPVVDCTCFGLP 60
 DB 1 MEROEERFKLAGRAIGKHLRLKROGAEETELSLADGRPTTQTRDDPPVVDCTCFGLP 60
 QY 61 RRIYIIMSGLGFCISFGIRCNLGVAVISVNNSTHRRGHVVOAQSPMBETVGLH 120
 DB 61 RRIYIIMSGLGFCISFGIRCNLGVAVISVNNSTHRRGHVVOAQSPMBETVGLH 120
 QY 121 GSEFMGVIYTOIPGGFICQKFAANRVGFAIVATSTLNLMLPSAAVHYGCYIPVAILLOG 180
 DB 121 GSEFMGVIYTOIPGGFICQKFAANRVGFAIVATSTLNLMLPSAAVHYGCYIPVAILLOG 180
 QY 181 IYEGVTTPACGCTGKAPPLERSRLATTAFCGSYAGAVVAVPLAGVLYVYSGMSVFVY 240
 DB 181 IYEGVTTPACGCTGKAPPLERSRLATTAFCGSYAGAVVAVPLAGVLYVYSGMSVFVY 240
 QY 241 YGSPFGFWTLFVLLVYESPALHPSISEERKYTEADIESAKLAMPPLKFSPPMRFT 300
 DB 241 YGSPFGFWTLFVLLVYESPALHPSISEERKYTEADIESAKLAMPPLKFSPPMRFT 300
 QY 301 SMPVVAIIYANFCRSWTFYLLISQPDYEEVGFSEISKVGLVSALPHLWMTIIVPIGQ 360
 DB 301 SMPVVAIIYANFCRSWTFYLLISQPDYEEVGFSEISKVGLVSALPHLWMTIIVPIGQ 360
 QY 361 IADFLSRIMSTTVNRKLMNCGFMEATLLIVGYSKGVASIFVLVANGFSGFALS 420

DB 361 IADFLSRIMSTTVNRKLMNCGFMEATLLIVGYSKGVASIFVLVANGFSGFALS 420
 QY 421 GENVNHLDIAPRYASILNGISNGVGLSGMCPPIVGAMTKKTEEMQYVPLASLVHY 480
 DB 421 GENVNHLDIAPRYASILNGISNGVGLSGMCPPIVGAMTKKTEEMQYVPLASLVHY 480
 QY 481 GGVITYGVFASGEKPPMAPEPMSSEKCGFVGHDLAAGSDSEMEDEAPPPAPPPPS 540
 DB 481 GGVITYGVFASGEKPPMAPEPMSSEKCGFVGHDLAAGSDSEMEDEAPPPAPPPPS 540
 QY 541 YGATSTPOPPRPPPPRDY 560
 DB 541 YGATSTPOPPRPPPPRDY 560

RESULT 7
 ID ADD01474 standard; protein; 560 AA.
 AC ADD01474;
 AC ADD01474;
 DT 01-JAN-2004 (first entry)
 DE Human VGLUT1 protein sequence.
 XX Human VGLUT1 protein sequence.
 XX antidiabetic; antihypertensive; antidiabetic; antihypertensive;
 XX neuroprotective; anabolic; antiinflammatory; immunosuppressive;
 XX cytoskeletal; antisthmatic; antiarthritic; cerebroprotective;
 XX antiallergic; dermatological; cardiant; antiParkinsonian; neuroleptic;
 XX glucose transporter; potassium ion channel protein; diabetes;
 XX hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
 XX colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
 XX sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
 XX meningitis; hepatitis; myocarditis; asthma; immune disorder;
 XX multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
 XX allergy; hay fever; allergic rhinitis; anaphylactic shock;
 XX atopic dermatitis; circulatory disorder; heart failure; cancer;
 XX Alzheimer's disease; Parkinson's disease; schizophrenia;
 XX hyperlactinemia; Cushing's disease; vesicular glutamate transporter.
 OS Homo sapiens.
 XX Homo sapiens.
 XX WO2003054190-A1.
 XX 03-JUL-2003.
 XX 19-DEC-2002; 2002WO-JP013290.
 XX 21-DEC-2001; 2001JP-00389361.
 XX 25-DEC-2001; 2001JP-00392577.
 XX 26-DEC-2001; 2001JP-00394947.
 XX 26-DEC-2001; 2001JP-00395467.
 XX 06-FEB-2002; 2002JP-00030010.
 XX 08-FEB-2002; 2002JP-00033095.
 XX 06-JUN-2002; 2002JP-00165336.
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX Nakanishi A, Sagiya Y, Uno Y;
 XX WPI, 2003-541817/51.
 XX Glucose transporter TCHO99, vesicular glutamate transporter TCH177 and
 XX potassium channel protein TCH136 and DNA encoding them for diagnosis,
 XX treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
 XX digestive disorders.
 XX Disclosure, Fig 3; 221pp; Japanese.
 XX The invention relates to a novel glucose transporter TCHO99, vesicular
 XX glutamate transporter TCH177 and voltage-dependent potassium ion channel
 XX protein TCH136. The sequences are useful in the treatment, prevention and
 XX diagnosis of a broad range of diseases including diabetes, hyperlipemia,

CC arteriosclerosis, digestive disorders (such as Crohn's disease, colitis, gastritis, ileitis and rectal inflammation), inflammatory diseases, sepsis, prostatic hypertrophy, reproductive disorders, pneumonia, meningitis, hepatitis, myocarditis, asthma, immune disorders (such as multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus), allergies (such as hay fever, allergic rhinitis, anaphylactic shock and atopic dermatitis), circulatory disorders (such as heart failure), cancer (such as cancer of the lung, kidney, liver, ovary, prostate, stomach, pancreas, bladder, breast, fallopian tubes or colon), central nervous system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and secretory disorders (such as hyperprolactinemia and Cushing's disease). This sequence represents the protein sequence for the human VGLUT1 glutamate transporter which was used for comparison with the novel human vesicular glutamate transporter TCH177.

CC Sequence 560 AA;

Query Match 99.7%; Score 2962; DB 7; Length 560;

Best Local Similarity 99.8%; Pred. No. 2.9e-266; Mismatches 1; Indels 0; Gaps 0;

Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFOEERKLAGALGKHLLEKROGATLELSADGRVTTQTRDPVVDCTCFGLP 60
 DB 1 MEFOEERKLAGALGKHLLEKROGATLELSADGRVTTQTRDPVVDCTCFGLP 60
 QY 61 RRYIIAINGSGFCISFGIRCNLGVAVSMVNNSTTHRGHVVOXKQFSWDPETVGLIH 120
 DB 61 RRYIIAINGSGFCISFGIRCNLGVAVSMVNNSTTHRGHVVOXKQFSWDPETVGLIH 120
 QY 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 180
 DB 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 180
 QY 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 180
 DB 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 180
 QY 181 LVEGVTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
 DB 181 LVEGVTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
 QY 241 YGSFGIFWYLFWLVSYESPALHPSISEBERKYIEDAIGESAKIMNPLTKFSTPMRRFT 300
 DB 241 YGSFGIFWYLFWLVSYESPALHPSISEBERKYIEDAIGESAKIMNPLTKFSTPMRRFT 300
 QY 301 SMPVYAIIVANFCRSMFTFYLLISQPDYFEEVFGFELSKVLVSALPHLVNTIIVPIGGQ 360
 DB 301 SMPVYAIIVANFCRSMFTFYLLISQPDYFEEVFGFELSKVLVSALPHLVNTIIVPIGGQ 360
 QY 361 IADFLRSRRIMSTNVKRLNCGGFGMEATLLLVGYSKGVASISFLVLAVGSFGFAIS 420
 DB 361 IADFLRSRRIMSTNVKRLNCGGFGMEATLLLVGYSKGVASISFLVLAVGSFGFAIS 420
 QY 421 GFNNHLDIAPRYASITMGISNGVGTLSGMVCPITVGMTHKTRREKQYVFLASLVHY 480
 DB 421 GFNNHLDIAPRYASITMGISNGVGTLSGMVCPITVGMTHKTRREKQYVFLASLVHY 480
 QY 481 GGVIFYGVAFSGEOPMAPEPEMSEKCGFVGHQDLAGSDSEMEDEALPGCAPPAPPS 540
 DB 481 GGVIFYGVAFSGEOPMAPEPEMSEKCGFVGHQDLAGSDSEMEDEALPGCAPPAPPS 540
 QY 541 YGATHSTFQPPRPVVDY 560
 DB 541 YGATHSTFQPPRPVVDY 560

RESULT 8

AAO13870 AAO13870 standard; protein; 567 AA.

XX AAO13870;

XX 06-NOV-2001 (first entry)

XX Human polypeptide SEQ ID NO 27762.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KV vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX WO200164835-A2.

XX 07-SEP-2001.

XX 26-FEB-2001; 2001WO-US004927.

XX 28-FEB-2000; 2000US-00515126.

XX 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

XX N-PSDB; AA193801.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 27762; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AAO00010-AAO13910) that exhibit actively elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcc_sequences

CC Sequence 567 AA;

Query Match 99.7%; Score 2962; DB 4; Length 567;

Best Local Similarity 99.8%; Pred. No. 2.9e-266; Mismatches 1; Indels 0; Gaps 0;

Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFOEERKLAGALGKHLLEKROGATLELSADGRVTTQTRDPVVDCTCFGLP 60
 DB 8 MEFOEERKLAGALGKHLLEKROGATLELSADGRVTTQTRDPVVDCTCFGLP 67
 QY 61 RRYIIAINGSGFCISFGIRCNLGVAVSMVNNSTTHRGHVVOXKQFSWDPETVGLIH 120
 DB 61 RRYIIAINGSGFCISFGIRCNLGVAVSMVNNSTTHRGHVVOXKQFSWDPETVGLIH 127
 QY 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 180
 DB 121 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 187
 QY 128 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 187
 DB 128 GSFFMGYIVTQIPGGFICQKFAANRVGFAIVASTLMLIPSAARVHYGCVIVRILQG 187
 QY 181 LVEGVTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
 DB 181 LVEGVTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 247
 QY 241 YGSFGIFWYLFWLVSYESPALHPSISEBERKYIEDAIGESAKIMNPLTKFSTPMRRFT 300
 DB 241 YGSFGIFWYLFWLVSYESPALHPSISEBERKYIEDAIGESAKIMNPLTKFSTPMRRFT 307
 QY 301 SMPVYAIIVANFCRSMFTFYLLISQPDYFEEVFGFELSKVLVSALPHLVNTIIVPIGGQ 360
 DB 301 SMPVYAIIVANFCRSMFTFYLLISQPDYFEEVFGFELSKVLVSALPHLVNTIIVPIGGQ 367
 QY 361 IADFLRSRRIMSTNVKRLNCGGFGMEATLLLVGYSKGVASISFLVLAVGSFGFAIS 420

Db	368	IADFLARSRIMSTVNRKTLNMGCGRMEATLLLVGYSHSKGAIVFLVAVFSGSPAS	427
Qy	421	GFNVNHLDIAPRYASIIIMGINSNGVGLTSGMVCPIIVGAMTKTKTREEMOVFLIASLVHY	480
Db	428	GFNVNHLDIAPRYASIIIMGINSNGVGLTSGMVCPIIVGAMTKTKTREEMOVFLIASLVHY	487
Qy	441	CGVITVGVAFASGEKQPMAPPEEMSEKCGFVGHDOLAGSDDSMEBAPPGAPAPAPPS	540
Db	488	GGVITVGVAFASGEKQPMAPPEEMSEKCGFVGHDOLAGSDDSMEBAPPGAPAPAPPS	547
Qy	541	YGATSTFQPPRPVVDY 560	
Db	548	YGATSTFQPPRPVVDY 567	
RESULT 9			
ABG74794			
ID	ABG74794	standard; protein; 560 AA.	
XX			
AC	ABG74794;		
XX			
DT	10-JUN-2003	(first entry)	
XX			
DE	Murine BNPI protein.		
XX			
KM	BNPI; sodium-dependent inorganic phosphate cotransporter; DNPI;		
KM	pain-regulation; glutamate transport mediator; musculo-skeletal pain;		
KM	brain sodium-dependent inorganic phosphate cotransporter; analgesic;		
KM	brain inorganic phosphate cotransporter; antimigraine; chronic pain;		
KM	differentiation-associated inorganic phosphate cotransporter; migraine;		
KM	neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;		
KM	visceral pain; cerebral pain; peripheral pain; inflammatory pain; murine;		
XX	cluster headache; trigeminal neuralgia; enzyme.		
XX			
OS	Mus musculus.		
XX			
FN	WO2002101394-A2.		
XX			
PD	19-DEC-2002.		
XX			
PF	13-JUN-2002; 2002MO-EP006484.		
XX			
XX	13-JUN-2001; 2001DE-01028541.		
PR			
XX			
PA	(CHEF) GRUENENTHAL GMBH.		
PI	Weihe E, Schaefer MK;		
XX			
XX			
XX	WPI; 2003-148835/14.		
DR	N-P5DB; ABX13552.		
XX			
PT	Identifying pain-regulating compounds, useful particularly for treating		
PT	chronic pain, based on interaction with specific phosphate		
PT	cotransporters.		
PS	Claim 1a; Fig 1h; 104dp; German.		
XX			
CC	This invention describes a novel method for identifying pain-regulating		
CC	substances. The method comprises incubating a test substance with BNPI		
CC	(brain sodium-dependent inorganic phosphate cotransporter) or DNPI		
CC	(differentiation-associated sodium-dependent inorganic phosphate		
CC	cotransporter then measuring either binding of the test substance to BNPI		
CC	or DNPI or some functional property of the proteins that is altered by		
CC	binding to the test substance. The novel pain-regulating substances have		
CC	analgesic and antimigraine activity. BNPI and DNPI are mediators of		
CC	glutamate transport. The products of the invention are used for treating		
CC	chronic pain, particularly musculo-skeletal, neuropathic (especially		
CC	allodynic pain, mechanical hyperalgesia or diabetic neuropathy),		
CC	visceral, cerebral, peripheral and/or inflammatory pain, also migraine,		
CC	cluster headache and trigeminal neuralgia. This sequence represents		
CC	murine BNPI polypeptide encoded by the polynucleotide (deposited in		
XX	XM_134342) in the method disclosed in the invention		
XX			

Seq	Sequence	560 AA;	98.6%;	Score 2929;	DB 6;	Length 560;
	Query Match		98.4%;	Pred. No. 3.4e-263;		
	Best Local Similarity		98.4%;	Pred. No. 3.4e-263;		
	Matches 551;	Conservative 5;	Mismatches 4;	Indels 0;	Gaps 0	
QY	1	MEFRQEEERKLAKGRALGTLHRLLEKROGAEFTLEISADGRPTTQTRDPVVDCTCFGLP				60
DB	1	MEFRQEEERKLAKGRALGTLHRLLEKROGAEFTLEISADGRPTTQTRDPVVDCTCFGLP				60
QY	61	RRYIIAISGSGLPFCISFGIRCLGVAIYSVMWNSTTHRGHVVQKAFSPMDPEVYGLIH				120
DB	61	RRYIIAISGSGLPFCISFGIRCLGVAIYSVMWNSTTHRGHVVQKAFSPMDPEVYGLIH				120
QY	121	GSPFWGVYIVTQIPGGFICQKFAANRVPFPAIVASTLMLIPSAARVHYGCVIPVRILOG				180
DB	121	GSPFWGVYIVTQIPGGFICQKFAANRVPFPAIVASTLMLIPSAARVHYGCVIPVRILOG				180
QY	181	LVEGVITYPACGIGMSKMAPPLERSLATTAFCGSAAGAVVAMPPLAGVLVQYSGMSSVFPV				240
DB	181	LVEGVITYPACGIGMSKMAPPLERSLATTAFCGSAAGAVVAMPPLAGVLVQYSGMSSVFPV				240
QY	241	YGSFGCIFMYLLFMILVSYSPALHPISISEERKYIDAIAGESAKLMNPPTKFTPMRRPFT				300
DB	241	YGSFGCIFMYLLFMILVSYSPALHPISISEERKYIDAIAGESAKLMNPPTKFTPMRRPFT				300
QY	301	SMPVYAIIVANFCRSMTFFYLLLSQPDYFEEVFGFEISKVLVSALPHLWMTIIVPIGQ				360
DB	301	SMPVYAIIVANFCRSMTFFYLLLSQPDYFEEVFGFEISKVLVSALPHLWMTIIVPIGQ				360
QY	361	IADFLRSRRIMSTTVKRLKLNCCGGFGMEATLLVVGYSHSKVAISFLVLAVGESEGPALS				420
DB	361	IADFLRSRRIMSTTVKRLKLNCCGGFGMEATLLVVGYSHSKVAISFLVLAVGESEGPALS				420
QY	421	GFNNVHLDIARVYASILMGISNGVYGLSGMCPPIVGAMTKTRKEEMQYVFLISLVHY				480
DB	421	GFNNVHLDIARVYASILMGISNGVYGLSGMCPPIVGAMTKTRKEEMQYVFLISLVHY				480
QY	481	GGVIFPVGFAPGAGEKQPMAPERPMSEKKGFGVGHDLASDSEMDDEAPPGAPAPPPS				540
DB	481	GGVIFPVGFAPGAGEKQPMAPERPMSEKKGFGVGHDLASDSEMDDEAPPGAPAPPPS				540
QY	541	YGATHSTFQPRPPPPVVDY 560				
DB	541	YGATHSTVQPRPPPPVVDY 560				
RESULT 10						
ID	ADCL5488					
XX	ADCL5488	standard; protein; 560 AA.				
XX	ADCL5488;					
DT	18-DEC-2003	(first entry)				
XX	Mouse BNPI protein.					
XX	BNPI; DNP1;					
KM	brain-associated sodium-dependent inorganic phosphate transporter;					
KM	differentiation-associated inorganic phosphate transporter;					
KM	ophthalmological; auditory; neuroleptic; antineuritic antidepressant;					
KM	cerebroprotective; neuroprotective; analgesic; anorectic; anticonvulsant;					
KM	antiparkinsonian; vasotropic; antileptic; antiarthritic; tranquilizer;					
KM	vinorelbine; antibacterial; protozoacide; antiinflammatory; cardiant;					
KM	hypotensive; antidiabetic; immunosuppressive; antidiabetic;					
KM	antialcoholic; anti-HIV; nootropic; antiallergic; gene therapy;					
KM	vision disorder; retinitis pigmentosa; optical degeneration;					
KM	hearing disorder; tinnitus; Meniere's disease; schizophrenia; mania;					
KM	depression; stroke; brain trauma; paralysis;					
KM	amyotrophic lateral sclerosis; neuralgia; weight regulation; obesity;					
KM	anorexia nervosa; epilepsy; hemiballism; Huntington chorea; stress;					
KM	Parkinson's disease; cataract; arthritis; hyperactivity;					
KM	developmental disorder; rabies; infection; influenza; malaria; CJD;					

KM inflammatory bowel disease; Crohn's disease; hypertension; toxoplasmosis;
 KM asthma; autoimmunity; neuropathy; diabetes; HIV; AIDS;
 KM autonomic disorder; digestive tract disorder; nervous system disorder;
 KM neurodegeneration; Alzheimer's disease; ischemia; encephalitis;
 KM prion disease; demyelination; multiple sclerosis; retinal degeneration;
 KM glioma; myeloma; retinal detachment; ataxia; memory disorder;
 KM cognitive disorder; stiff-man syndrome; restless leg syndrome; phobia;
 KM sleep disorder; neurotoxicological disease; spinal motor neuron disease;
 KM muscular atrophy; neuroinflammation; fever; taste disorder; food allergy;
 KM aggression; paraneoplastic neuroendocrine disorder; Tourette syndrome;
 KM sudden infant death syndrome; cardiac infarct; insomnia; amnesia;
 KM multiple sclerosis; jet lag; sexual dysfunction; impotence; priapism;
 KM neuroprotection; enzyme.
 XX Mus sp.
 OS WO2003029828-A2.
 XX 10-APR-2003.
 PD 24-SEP-2002; 2002MO-EP010707.
 XX 24-SEP-2001; 2001DE-01047006.
 PR 25-SEP-2001; 2001DE-01047028.
 XX (CHEF) GRUENENTHAL GMBH.
 PA Weihe E, Schaefer MK;
 XX WPI; 2003-354751/33.
 DR WPI; 2003-354751/33.
 XX Identifying agents for treatment and diagnosis of disease, e.g.
 PT depression or viral infections, from binding to inorganic phosphate
 PT transporters, also new agents.
 PT Claim 1; Fig 1h; 129p; German.
 PS This invention describes a novel method of identifying agents for
 XX detection or treatment of specified conditions. The method comprises
 CC incubating test compound with BNP1 or DNP1 (brain or differentiation-
 CC associated sodium-dependent inorganic phosphate transporter), or related
 CC proteins, nucleic acids or cells (and/or cell preparations), then
 CC measuring binding of test compound or some functional parameter altered
 CC by binding. The products of the invention have ophthalmological,
 CC auditory, neuroleptic, anti-manic, antidepressant, cerebroprotective,
 CC neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
 CC vasotrophic, antiemetic, antiarthritic, tranquilizer, vitruclide,
 CC antibacterial, protozoacide, antiinflammatory, cardiac, hypotensive,
 CC antiaesthetic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
 CC nootropic and antiallergic activity. The method is used to identify
 CC agents for diagnosis and treatment (including gene therapy) of disorders
 CC of vision; retinitis pigmentosa; optical degeneration; hearing disorders
 CC or loss; tinnitus; Meniere's disease; schizophrenia; mania; depression;
 CC stroke; brain trauma; 'cut-through' paralysis; amyotrophic lateral
 CC sclerosis; neuralgia; weight regulation; obesity; anorexia nervosa;
 CC epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;
 CC transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
 CC cataract; arthritis; hyperactivity; developmental disorders; rabies;
 CC bacterial and viral infections; influenza; malaria; CJD; inflammatory
 CC bowel disease; Crohn's disease; cardio-vascular and -respiratory
 CC functional disorders; hypertension; baroreflex and chemoreflex
 CC diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
 CC nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
 CC HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
 CC systems; overexcitability, particularly mediated by glutamate;
 CC neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
 CC bacterial, Rasmussen or HIV); prion diseases; demyelination
 CC (particularly multiple sclerosis); retinal degeneration; glioma;
 CC myeloma; retinal detachment; diseases of cerebellum (ataxia); basal
 CC ganglia, pallidum, hearing or balancing organs; auditory canal; memory,
 CC learning and cognitive disorders; stiff-man or restless leg syndromes;
 CC anxiety; phobia; sleep disorders; drug dependency; addiction or
 CC withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);

CC hepatocellularopathy, with or without alcohol intoxication;
 CC neurotoxicological diseases; spinal motor neuron diseases; muscular
 CC atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
 CC taste disorders; food allergies; Chinese restaurant syndrome; aggression;
 CC paraneoplastic; tremor; neuroendocrine disorders; Tourette syndrome;
 CC cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis;
 CC burn-out syndrome; sudden infant death syndrome; cardiac infarct;
 CC insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
 CC dysfunction (impotence, priapism); also promotion of microglial activity,
 CC learning, cognition or memory; neuroprotection; diagnosis of neurostatic
 CC disease, and as adjuvant therapy for electrostimulation of the
 CC subthalamic nucleus in Parkinson's disease. This sequence represents the
 CC mouse BNP1 protein also represented in AN: XM_133432.
 XX

Sequence 560 AA;

Query Match 98.6%; Score 2929; DB 7; Length 560;

Best Local Similarity 98.4%; Pred. No. 3.4e-263; Matches 551; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY	1	MEFROEERKLAGRALGRLHLEKROGARTLEISADGRVYTTOTRPPVVDCTCFGLP	60
DB	1	MEFROEERKLAGRALGRLHLEKROGARTLEISADGRVYTTOTRPPVVDCTCFGLP	60
QY	61	RRYIAIMSGLGFCSIFGIRCNLGAIVSMNNSTTHRGHVVOXQAFSMDPETVGLH	120
DB	61	RRYIAIMSGLGFCSIFGIRCNLGAIVSMNNSTTHRGHVVOXQAFSMDPETVGLH	120
QY	121	GSFPMGYLVTOIPGAFICQKFAANRVFQFAIVATSTLMLIPSAARVYGCIVFRIILOG	180
DB	121	GSFPMGYLVTOIPGAFICQKFAANRVFQFAIVATSTLMLIPSAARVYGCIVFRIILOG	180
QY	181	LVEGVTYPACHGINSKMAPLERSRLATTAFCSYAGAVVAMPAGVLVOYSGMSVRYV	240
DB	181	LVEGVTYPACHGINSKMAPLERSRLATTAFCSYAGAVVAMPAGVLVOYSGMSVRYV	240
QY	241	YGSFGIFMYLFWLIVSVSPPLHPSISEERKYEDALGESAKLMNPLTKFSTPERRFT	300
DB	241	YGSFGIFMYLFWLIVSVSPPLHPSISEERKYEDALGESAKLMNPLTKFSTPERRFT	300
QY	301	SMPVYAIIVANFCRSWTFYLLISQPDVFEFVFGEISKVLVSNLPHLWNTIIVPICGQ	360
DB	301	SMPVYAIIVANFCRSWTFYLLISQPDVFEFVFGEISKVLVSNLPHLWNTIIVPICGQ	360
QY	361	IADFLRSRINSTNVRKLNCGFGEATLLLVGSHSGVAISFLVLAVSGSFAIS	420
DB	361	IADFLRSRINSTNVRKLNCGFGEATLLLVGSHSGVAISFLVLAVSGSFAIS	420
QY	421	GFNNVHLDIARVYASILMGISNGVGTLSGMTCPIIVGAMTKRREKQVYFLASLVHY	480
DB	421	GFNNVHLDIARVYASILMGISNGVGTLSGMTCPIIVGAMTKRREKQVYFLASLVHY	480
QY	481	GGVIFVGFASGEQPMAPPEMSEBCKGFVGHQOLAGSDSEMEDAEPGAPAPPPS	540
DB	481	GGVIFVGFASGEQPMAPPEMSEBCKGFVGHQOLAGSDSEMEDAEPGAPAPPPS	540
QY	541	YGATHSTVQPPRPPPVADY 560	
DB	541	YGATHSTVQPPRPPPVADY 560	

RESULT 11

ID ABG74793 standard; protein, 560 AA.

XX ABG74793;

XX 10-JUN-2003 (first entry)

XX Rat BNP1 protein.

KM BNP1; sodium-dependent inorganic phosphate cotransporter; DNP1; pain-regulation; glutamate transport mediator; musculo-skeletal pain;

PI Weihe E, Schaefer MK;
 XX WPI: 2003-354751/33.
 DR N-PSDB; ADCl5485.
 XX
 PT Identifying agents for treatment and diagnosis of diseases, e.g.
 XX depression or viral infections, from binding to inorganic phosphate
 XX transporters, also new agents.
 PS
 XX Claim 1; Fig 1f; 129pp; German.

This invention describes a novel method of identifying agents for
 CC detection or treatment of specified conditions. The method comprises
 CC incubating test compound with BNPI or DNPI (brain or differentiation-
 CC associated sodium-dependent inorganic phosphate transporter), or related
 CC proteins, nucleic acids or cells (and/or cell preparations), then
 CC measuring binding of test compound or some functional parameter altered
 CC by binding. The products of the invention have ophthalmological,
 CC auditory, neuroleptic, antianemic, antidepressant, cerebroprotective,
 CC neuroprotective, analgesic, anorectic, anticonvulsant, antiparkinsonian,
 CC vasotropic, antiemetic, antiarthritic, tranquilizer, vitruclide,
 CC antidiabetic, antiparasitic, antiinflammatory, cardiant, hypotensive,
 CC antiaesthetic, immunosuppressive, antidiabetic, antialcoholic, anti-HIV,
 CC neurotropic and antiallergic activity. The method is used to identify
 CC agents for diagnosis and treatment (including gene therapy) of disorders
 CC of vision, retinitis pigmentosa, optical degeneration, hearing disorders
 CC or loss, tinnitus, Meniere's disease, schizophrenia, mania, depression,
 CC stroke, brain trauma, 'cut-through' paralysis, amyotrophic lateral
 CC sclerosis, neuralgia, weight regulation, obesity, anorexia nervosa;
 CC epilepsy; hemiballism; Huntington chorea; stress; Parkinson's disease;
 CC transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness;
 CC caracact; arthritis; hyperactivity; developmental disorders; rabies;
 CC bacterial and viral infections; influenza; malaria; CJD; inflammatory
 CC bowel disease; Crohn's disease; cardio-vascular and -respiratory
 CC functional disorders; hypertension; baroreflex and chemoreflex
 CC diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral
 CC nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes;
 CC HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous
 CC systems; overexcitability, particularly mediated by glutamate;
 CC neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral,
 CC bacterial, Rasmussen or HIV); prion diseases; demyelination
 CC (particularly multiple sclerosis); retinal degeneration; glaucoma;
 CC nystagmus; retinal detachment; diseases of cerebellum (ataxia), basal
 CC ganglia, pallidum, hearing or balancing organs, auditory canal; memory,
 CC learning and cognitive disorders; stiff-man or restless leg syndromes;
 CC anxiety; phobia; sleep disorders; drug dependency, addiction or
 CC withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine);
 CC hepatocellularopathy, with or without alcohol intoxication;
 CC neurooncological diseases; spinal motor neuron diseases; muscular
 CC atrophy or dystrophy; spinal cord disease; neuroinflammation; fever;
 CC taste disorders; food allergies; Chinese restaurant syndrome; aggression;
 CC paraneoplasia; tremors; neuroendocrine disorders; Tourette syndrome;
 CC cerebrotendinous spasms; neuronal apoptosis or necrosis; astrocytosis;
 CC burn-out syndrome; sudden infant death syndrome; cardiac infarct;
 CC insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual
 CC dysfunction (impotence, priapism); also promotion of microglial activity,
 CC learning, cognition or memory; neuroprotection; diagnosis of neurostatic
 CC disease, and as adjuvant therapy for electrostimulation of the
 CC subthalamic nucleus in Parkinson's disease. This sequence represents the
 CC rat BNPI protein also represented in AN: U07609.
 XX

Sequence 560 AA;

Query Match 98.5%; Score 2925; DB 7; Length 560;
 Best Local Similarity 98.2%; Pred. No. 8e-263;
 Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEFROEERKLAGALGTLHLLEKROGARTLELSAAGRVTYOTRPPPVVDCCTCFGLP 60
 DB 1 MEFROEERKLAGALGTLHLLEKROGARTLELSAAGRVTYOTRPPPVVDCCTCFGLP 60
 QY 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOAKQFNMDDPETVGLIH 120
 |||

DB 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOAKQFNMDDPETVGLIH 120
 QY 121 GSFPMGYIVVOIRPGFICQKFAANRVGFALVAISTNNMLPSARVHYGCVIFRILQG 180
 DB 121 GSFPMGYIVVOIRPGFICQKFAANRVGFALVAISTNNMLPSARVHYGCVIFRILQG 180
 QY 181 LVEGVTPACGIMSKAPPLERSRLATTAFCGSGYAGVAVMPLAGVLVOYSGMSVFFV 240
 DB 181 LVEGVTPACGIMSKAPPLERSRLATTAFCGSGYAGVAVMPLAGVLVOYSGMSVFFV 240
 QY 241 YGSFGIFMYLFWLLVSVSPALPSPISEERKYTEIDAIGSAKMLPDKFTSTPARRFT 300
 DB 241 YGSFGIFMYLFWLLVSVSPALPSPISEERKYTEIDAIGSAKMLPDKFTSTPARRFT 300
 QY 301 SMPYVAIIIVANFGCSWTFYLLIIQPDYFEVRFPEISKVLGVALPMLVNTIIVPGGQ 360
 DB 301 SMPYVAIIIVANFGCSWTFYLLIIQPDYFEVRFPEISKVLGVALPMLVNTIIVPGGQ 360
 QY 361 IADFLRSRIMSTNNVRKLMNCGGFGMEATLLVVGSHSGVAISPLVLAVSGFAIS 420
 DB 361 IADFLRSRIMSTNNVRKLMNCGGFGMEATLLVVGSHSGVAISPLVLAVSGFAIS 420
 QY 421 GFNVNHLDIAPRYASIIIMGINSGVGTLSGWCPIIVGAMTKRREMOYVFLIASLVHY 480
 DB 421 GFNVNHLDIAPRYASIIIMGINSGVGTLSGWCPIIVGAMTKRREMOYVFLIASLVHY 480
 QY 481 GGVIFGYFAGSGEQPAPEPEMESEKGFVGHQVLGSDSEMEDEPPGAPAPAPPS 540
 DB 481 GGVIFGYFAGSGEQPAPEPEMESEKGFVGHQVLGSDSEMEDEPPGAPAPAPPS 540
 QY 541 YGATHSTFQPPRPPPPVVDY 560
 DB 541 YGATHSTFQPPRPPPPVVDY 560

RESULT 13

ID ABG74795 standard; protein, 562 AA.

AC ABG74795;

DT 10-JUN-2003 (first entry)

DE Human DNPI protein.

XX BNPI, sodium-dependent inorganic phosphate cotransporter; DNPI;
 KW brain-regulation; glutamate transport mediator; musculo-skeletal pain;
 KW brain sodium-dependent inorganic phosphate cotransporter; analgesic;
 KW brain inorganic phosphate cotransporter; antimigraine; chronic pain;
 KW differentiation-associated inorganic phosphate cotransporter; migraine;
 KW neuropathy; allodynic pain; mechanical hyperalgesia; diabetic neuropathy;
 KW visceral pain; cerebral pain; peripheral pain; inflammatory pain; human;
 KW cluster headache; trigeminal neuralgia; enzyme.

OS Homo sapiens.

EN WO2002101394-A2.

PD 19-DEC-2002.

PE 13-JUN-2002; 2002WO-EP006484.

PR 13-JUN-2001; 2001DE-01028541.

PA (CHBP) GRUENENTHAL GMBH.

PI Weihe E, Schaefer MK;

XX WPI: 2003-148835/14.

DR N-PSDB; ABX15553.

PT Identifying pain-regulating compounds, useful particularly for treating
 chronic pain, based on interaction with specific phosphate

transient ischemic attacks; emesis (e.g. after chemotherapy); dizziness; cataract; arthritis; hyperactivity; developmental disorders; rabies; bacterial and viral infections; influenza; malaria; CVD; inflammatory bowel disease; Crohn's disease; cardio-vascular and -respiratory functional disorders; hypertension; baroafferent and chemoafferent diseases; toxoplasmosis; asthma; autoimmunity in central and peripheral nervous systems; diabetic or alcoholic neuropathy; autoimmune diabetes; HIV-neuro-AIDS; disorders of the autonomic or digestive tract nervous systems; overexcitability, particularly mediated by glutamate; neurodegeneration; Alzheimer's disease; ischemia; encephalitis (viral, bacterial, Reussen or HIV); prion diseases; demyelination (particularly multiple sclerosis); retinal degeneration; glaucoma; myasthenia; retinal detachment; diseases of cerebellum (ataxia), basal ganglia, pallidum, hearing or balancing organs, auditory canal; memory, learning and cognitive disorders; stiff-man or restless leg syndromes; anxiety, phobia; sleep disorders; drug dependency, addiction or withdrawal (especially alcohol, nicotine, opiates, ecstasy or cocaine); hepatocellular carcinoma; with or without alcohol intoxication; neurotoxicological diseases; spinal motor neuron diseases; muscular atrophy or dystrophy; spinal cord disease; neuroinflammation; fever; taste disorders; food allergies; Chinese restaurant syndrome; aggression; paraneoplasia; tremors; neuroendocrine disorders; Tourette syndrome; cerebrovascular spasms; neuronal apoptosis or necrosis; astrocytosis; burn-out syndrome; sudden infant death syndrome; cardiac infarct; insomnia; retrograde amnesia; multiple sclerosis; jet lag; sexual dysfunction (impotence; priapism); also promotion of microglial activity, learning, cognition or memory; neuroprotection; diagnosis of neurostatic disease, and as adjuvant therapy for electrostimulation of the subthalamic nucleus in Parkinson's disease. This sequence represents the human DNPI protein described in the disclosure of the invention.

Sequence 582 AA:

Query Match 78.0%; Score 2317.5; DB 7; Length 582;
Best Local Similarity 79.4%; Pred. No. 2.7e-206;
Matches 429; Conservative 56; Mismatches 50; Indels 5; Gaps 2;

5 QEERKALGKRLKRLKROGAEETLSDGRPTTQTRDPVVDCTCFGLPRRYI 64
13 KEGLNFKGSLGQYRVRLEKKQDGTETLEDEKPLEPERKAPLDCCTCFGLPRRYI 72
65 IAINSGFGFCSIFGRNMGVAIVSMVNSSTHRRGHVVVOKAFSPDPTVGLHSGFF 124
73 IAINSGFGFCSIFGRNMGVAIVSMVNSSTHRRGHVVVOKAFSPDPTVGLHSGFF 132
125 WGYIVTQIPGFCIQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFRILQGLVEG 184
133 WGYIVTQIPGFCIQKFAANRVGFAIVATSTLNLIPSAARVHVCVIFRILQGLVEG 192
185 VTYRACHGINKMAPLERSRLATTAFCGSAAGVAVNMAPLACVLYVCGSGSVPVVSGF 244
193 VTYRACHGINKMAPLERSRLATTAFCGSAAGVAVNMAPLACVLYVCGSGSVPVVSGF 252
245 GTFWYLFMLVSYESPALPISIEERKYEIDALGESAKMLNPLTKFTPMRRFPTSPV 304
253 GFWYLFMLVSYESPALPISIEERKYEIDALGESAKMLNPLTKFTPMRRFPTSPV 312
305 YAIIVANFCRSWTFYLLISQPDYEEVFGFEISKVGLVSLPMLWMTIIVIGQIADF 364
313 YAIIVANFCRSWTFYLLISQPDYEEVFGFEISKVGLVSLPMLWMTIIVIGQIADF 372
365 LRSKRIMSTNVKRLKMGCGFGMEKTLVLYVGYSHSKVAISFLVANGFSGFALSQNV 424
373 LRSKRIMSTNVKRLKMGCGFGMEKTLVLYVGYSHSKVAISFLVANGFSGFALSQNV 432
425 NMLDAPRYASTLNGISNGVGLTSMVCPITIVGATKTKTEBEMOYVLLASLVHGGVI 484
433 NMLDAPRYASTLNGISNGVGLTSMVCPITIVGATKTKTEBEMOYVLLASLVHGGVI 492
485 FYGVAFSGEKQPMABEEMSEKCGFVGHDLQAGSDSEMEDEABPPAPAPPPSYGAT 544
493 FYGVAFSGEKQPMABEEMSEKCGFVGHDLQAGSDSEMEDEABPPAPAPPPSYGAT 547

RESULT 15
ADD01475
ID ADD01475 standard; protein: 582 AA.
XX AC ADD01475;
XX . . .
DT 01-JAN-2004 (first entry)
XX
XX Human VGLUT2 protein sequence.
XX
XX antidiabetic; antilipemic; antiarteriosclerotic; nootropic;
XX neuroprotective; anabolic; antiinflammatory; immunosuppressive;
XX cytoskeletal; antistatic; antiarthritic; cerebroprotective;
XX antiallergic; dermatological; cardiac; antiParkinsonian; neuroleptic;
XX glucose transporter; potassium ion channel protein; diabetes;
XX hyperlipemia; arteriosclerosis; digestive disorder; Crohn's disease;
XX colitis; gastritis; ileitis; rectal inflammation; inflammatory disease;
XX sepsis; prostatic hypertrophy; reproductive disorder; pneumonia;
XX meningitis; hepatitis; myocarditis; asthma; immune disorder;
XX multiple sclerosis; rheumatoid arthritis; Sjogren's disease; lupus;
XX allergy; hay fever; allergic rhinitis; anaphylactic shock;
XX atopic dermatitis; circulatory disorder; heart failure; cancer;
XX Alzheimer's disease; Parkinson's disease; schizophrenia;
XX hyperprolactinemia; Cushing's disease; vesicular glutamate transporter.
XX Homo sapiens.
XX
XX WO2003054190-A1.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-JP013290.
XX
XX 21-DEC-2001; 2001JP-00389361.
XX 25-DEC-2001; 2001JP-00392577.
XX 26-DEC-2001; 2001JP-00394947.
XX 26-DEC-2001; 2001JP-00395467.
XX 06-FEB-2002; 2002JP-00030010.
XX 08-FEB-2002; 2002JP-00033095.
XX 06-JUN-2002; 2002JP-00165336.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Nakanishi A, Sagiya Y, Uno Y;
XX
XX WPI; 2003-541817/51.
XX
XX Glucose transporter TCH099, vesicular glutamate transporter TCH177 and
XX potassium channel protein TCH136 and DNA encoding them for diagnosis,
XX treatment and prevention of diabetes, hyperlipemia, arteriosclerosis and
XX digestive disorders.
XX
XX Disclosure; Fig 3; 221pp; Japanese.
XX
XX The invention relates to a novel glucose transporter TCH099, vesicular
XX glutamate transporter TCH177 and voltage-dependent potassium ion channel
XX protein TCH136. The sequences are useful in the treatment, prevention and
XX diagnosis of a broad range of diseases including diabetes, hyperlipemia,
XX arteriosclerosis, digestive disorders (such as Crohn's disease, colitis,
XX gastritis, ileitis and rectal inflammation), inflammatory diseases,
XX sepsis, prostatic hypertrophy, reproductive disorders, pneumonia,
XX meningitis, hepatitis, myocarditis, asthma, immune disorders (such as
XX multiple sclerosis, rheumatoid arthritis, Sjogren's disease and lupus),
XX allergies (such as hay fever, allergic rhinitis, anaphylactic shock and
XX atopic dermatitis), circulatory disorders (such as heart failure), cancer
XX (such as cancer of the lung, kidney, liver, ovary, prostate, stomach,
XX pancreas, bladder, breast, fallopian tubes or colon), central nervous
XX system diseases (such as Alzheimer's, Parkinson's and schizophrenia) and
XX secretory disorders (such hyperprolactinemia and Cushing's disease). This
XX sequence represents the protein sequence for the human VGLUT2 glutamate
XX transporter which was used for comparison with the novel human vesicular
XX glutamate transporter TCH177.

XX Sequence 582 AA;
SQ

Query Match 78.0%; Score 2317.5; DB 7; Length 582;
Best Local Similarity 79.4%; Pred. No. 2,7e-206;
Matches 429; Conservative 56; Mismatches 50; Indels 5; Gaps 2;

```
QY 5 QEBFRKLARALGKLRLLLEKROGAETLELSADGRPVTTQTRDPVPVDCFCGLPRRYI 64
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 KEGLNKFAKSLGQIYRVLEKKQDTGETTELTEDEGKPLEVPERKAPLDCCTCFGLPRRYI 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 65 IAIMSGLGFICISGIRCNIGVAIVSMVNNSTTHRGHVVQKQPSMDPETGLHGSFF 124
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 IAIMSGLGFICISGIRCNIGVAIVDMVNNSTTHRGKVIKKAKEFNWDEPTVGMHGSFF 132
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 125 WGIYVTOIPGGFICQKFAANRVGFALIVATSTLNMILPSAARVHYGCVIFVRILQGLVEG 184
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 WGIYITQIPGGYIASRLAANRVGAAILITSTLNMILPSAARVHYGCVIFVRILQGLVEG 192
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 185 VTYYPACHGIMSKWAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLYQSGMSSVFYVYGSF 244
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 VTYYPACHGIMSKWAPPLERSRLATTSFCGSYAGAVIAMPPLAGILVQYTGMSVVFYVYGSF 252
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 245 GLEFWYLFMLLVSYESPALHPISIEERKXTIEDAIGESAKLMPLTKESTPMRRPFTSMPV 304
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 GNVWYWFMLLVSYESPAPKHPITIDEERRYIEESIGESANMLGAMERKFTPMRKFFTSMPV 312
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 305 YAIIVANFCRSMTFYLLISOPDYFEEVGFETISKVGLVSALPHLVMTTIIVPIGQIADF 364
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 YAIIVANFCRSMTFYLLISQPAYFEEVGFETISKVGMLSAVPHLVMTTIIVPIGQIADF 372
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 365 LRSRRI MSTTVNRKLNKCGFGMEATLLLVGYSHSKGVASIFLVLA VSGSGFAISGENV 424
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 373 LRSKQITLSTTVRKINCCGFGMEATLLLVGYSHTRGVAISFLVLA VSGSGFAISGFNV 432
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 425 NHDIA PRYASTIMGINSNGVTLISGMVCPILVGMATKHTREMOVYFLLASLVHYGVI 484
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 NHDIA PRYASTILMIGINSNGVTLISGMVCPILVGMATKNSREMOVYFLLAALVHYGVI 492
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 485 FYGVFASGEKOPWAEPEEMSEKCGFVGHDLAGSDSEMEDAEPPGAPAPAPPSYGAT 544
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 493 FYAIPASGEKQPMADPEETSEKCGFIHDEL----DEETGDI TQ-NYINVTGTSYGAT 547
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: June 2, 2005, 11:28:34
Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:25:48 ; Search time 479 Seconds

(without alignments)
1365.519 Million cell updates/sec

Title: US-10-734-731-4

Perfect score: 2970
Sequence: 1 MEFRQEFRLKAGRALGKLN.....YGAHTSTFPQPPPPVRYD 560

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 116806243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents_AA Main:*

1: /cgn2_6/ptodata/1/paa/US06_PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep.*
25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US105_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
33: /cgn2_6/ptodata/1/paa/US107_COMB.pep.*
34: /cgn2_6/ptodata/1/paa/US108_COMB.pep.*
35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
36: /cgn2_6/ptodata/1/paa/US110_COMB.pep.*
37: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2970	100.0	560	US-08-430-033-2	Sequence 2, Appli
2	2970	100.0	560	US-10-734-731-4	Sequence 4, Appli
3	2970	100.0	560	US-10-807-500-4	Sequence 4, Appli
4	2967	99.9	560	PCT-US98-02875-5	Sequence 5, Appli
5	2967	99.9	560	PCT-US98-02875A-5	Sequence 5, Appli
6	2967	99.9	560	US-09-380-164-5	Sequence 5, Appli
7	2967	99.9	560	US-10-314-790-5	GENERAL INFORMA
8	2967	99.9	560	US-60-039-462-5	Sequence 5, Appli
9	2962	99.7	560	US-10-170-205E-18690	Sequence 18690, A
10	2962	99.7	560	US-10-734-731-2	Sequence 2, Appli
11	2962	99.7	560	US-10-756-149-5598	Sequence 5598, Ap
12	2962	99.7	560	US-10-807-500-2	Sequence 2, Appli
13	2962	99.7	560	US-60-452-680-12892	Sequence 12892, A
14	2962	99.7	560	US-60-453-050-8103	Sequence 8103, Ap
15	2962	99.7	560	US-60-453-135-8103	Sequence 8103, Ap
16	2962	99.7	560	US-60-466-412-8103	Sequence 8103, Ap
17	2962	99.7	567	US-10-320-366A-27762	Sequence 27762, A
18	2962	99.7	567	US-10-940-774-11354	Sequence 11354, A
19	2929	98.6	560	US-10-734-731-8	Sequence 8, Appli
20	2929	98.6	560	US-10-807-500-8	Sequence 8, Appli
21	2925	98.5	560	US-09-965-522-4	Sequence 4, Appli
22	2925	98.5	560	US-09-991-212-4	Sequence 4, Appli
23	2925	98.5	560	US-09-991-212A-4	Sequence 4, Appli
24	2925	98.5	560	US-10-734-731-6	Sequence 6, Appli
25	2925	98.5	560	US-10-807-500-6	Sequence 6, Appli
26	2925	98.5	560	US-10-807-500-6	Sequence 6, Appli
27	2317.5	78.0	582	US-10-877-818-4	Sequence 4, Appli
28	2317.5	78.0	582	US-10-170-205E-23413	Sequence 23413, A
29	2317.5	78.0	582	US-10-734-731-10	Sequence 10, Appli
30	2313.5	77.9	578	US-10-807-500-10	Sequence 10, Appli
31	2313.5	77.9	582	US-10-389-967-4	Sequence 4, Appli
32	2313.5	77.9	582	US-10-205-331-7	Sequence 7, Appli
33	2313.5	77.9	582	US-10-734-731-12	Sequence 12, Appli
34	2313.5	77.9	582	US-10-734-731-14	Sequence 14, Appli
35	2313.5	77.9	582	US-10-807-500-12	Sequence 12, Appli
36	2307.5	77.7	582	US-10-807-500-14	Sequence 14, Appli
37	2307.5	77.7	582	PCT-US01-04098A-1935	Sequence 1935, Ap
38	2307.5	77.7	582	US-10-258-899A-1935	Sequence 1935, Ap
39	2185	73.6	589	US-10-293-244-1935	Sequence 2, Appli
40	2185	73.6	589	PCT-US02-39565-2	Sequence 2, Appli
41	2185	73.6	589	US-10-389-967-2	Sequence 28, Appli
42	2185	73.6	589	US-10-499-731-28	Sequence 3527, Ap
43	2154.5	72.5	601	US-10-777-288A-3527	Sequence 46, Appli
44	2138.5	72.0	566	US-10-499-731-46	Sequence 300, App
45	2138.5	72.0	566	PCT-US02-35464-300	Sequence 300, App
			566	US-10-287-226-300	

ALIGNMENTS

RESULT 1
US-08-430-033-2
Sequence 2, Application US/08430033

GENERAL INFORMATION:
APPLICANT: Ni, Binhui
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,033
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-10006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-430-033-2

```

```

Query Match      100.0%; Score 2970; DB 8; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.8e-272;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MEFROEERKLAGRALGKLRLLERKQGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKLRLLERKQGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
DB 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
DB 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
DB 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
QY 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
DB 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
QY 181 LVEGVTYPACHIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSVEFY 240
DB 181 LVEGVTYPACHIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSVEFY 240
QY 241 YGSFGIFWYLFWLIVSYESPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
DB 241 YGSFGIFWYLFWLIVSYESPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
QY 301 SMPVVAIIYANFCRSMWTFYLLISQPDYEEVFGFEISKGLVSLPPLVMTIIVPIGQ 360
DB 301 SMPVVAIIYANFCRSMWTFYLLISQPDYEEVFGFEISKGLVSLPPLVMTIIVPIGQ 360
QY 361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAAGSGFALS 420
DB 361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAAGSGFALS 420
QY 421 GENVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKKTRBEMQYVFLIASLVHY 480
DB 421 GENVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKKTRBEMQYVFLIASLVHY 480
QY 481 GGVTFYGVFASGEKQPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
DB 481 GGVTFYGVFASGEKQPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATHSTFOPRPPRPVVDY 560
DB 541 YGATHSTFOPRPPRPVVDY 560

```

```

RESULT 2
US-10-734-731-4
; Sequence 4, Application US/10734731
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING METHOD USING BNPI AND DNPI

```

```

; FILE REFERENCE: 029310.52995US
; CURRENT APPLICATION NUMBER: US/10/734,731
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: PCT/EP02/06484
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: DE 101 28 541.8
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-731-4

```

```

Query Match      100.0%; Score 2970; DB 33; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.8e-272;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MEFROEERKLAGRALGKLRLLERKQGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKLRLLERKQGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
DB 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
DB 61 RRYIIAINGSLGFCISFGIRCNLGVAIYSMVNNSSTTHRGHVVOQAQPSMDPEVGLIH 120
QY 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
DB 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
QY 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
DB 121 GSFPMGYIYQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHVCVIFVRILOG 180
QY 181 LVEGVTYPACHIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSVEFY 240
DB 181 LVEGVTYPACHIGWSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSVEFY 240
QY 241 YGSFGIFWYLFWLIVSYESPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
DB 241 YGSFGIFWYLFWLIVSYESPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
QY 301 SMPVVAIIYANFCRSMWTFYLLISQPDYEEVFGFEISKGLVSLPPLVMTIIVPIGQ 360
DB 301 SMPVVAIIYANFCRSMWTFYLLISQPDYEEVFGFEISKGLVSLPPLVMTIIVPIGQ 360
QY 361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAAGSGFALS 420
DB 361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAAGSGFALS 420
QY 421 GENVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKKTRBEMQYVFLIASLVHY 480
DB 421 GENVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKKTRBEMQYVFLIASLVHY 480
QY 481 GGVTFYGVFASGEKQPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
DB 481 GGVTFYGVFASGEKQPMAPPEEMSEKCGFVGHDLAAGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATHSTFOPRPPRPVVDY 560
DB 541 YGATHSTFOPRPPRPVVDY 560

```

```

RESULT 3
US-10-807-500-4
; Sequence 4, Application US/10807500
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING PROCESS FOR VARIOUS INDICATIONS USING BNPI AND/OR DNPI
; FILE REFERENCE: 029310.53352US
; CURRENT APPLICATION NUMBER: US/10/807,500
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/EP02/10707
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 006.1

```

PRIOR FILING DATE: 2001-09-24
 PRIOR APPLICATION NUMBER: DE 101 47 028.2
 PRIOR FILING DATE: 2001-09-25
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO: 4
 LENGTH: 560
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-807-500-4

Query Match 100.0%; Score 2970; DB 34; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.8e-272;
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEFROEERKLAGRALGKHLRLERKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKHLRLERKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAINGSGFCISFGIRCNLGAIVSMVNNSTTHRGHVVOKAFSMDPETVGLIH 120
DB 61 RRYIIAINGSGFCISFGIRCNLGAIVSMVNNSTTHRGHVVOKAFSMDPETVGLIH 120
QY 121 GSFPMGYIVTOIPGSGFCOKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRIIOG 180
DB 121 GSFPMGYIVTOIPGSGFCOKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRIIOG 180
QY 181 LVEGTVYACGIGMSKMAPLERSLATTAFCGSYAGAVVAMPAGLVVOYSGMSSVRYV 240
DB 181 LVEGTVYACGIGMSKMAPLERSLATTAFCGSYAGAVVAMPAGLVVOYSGMSSVRYV 240
QY 241 YGSFGIFWYLFMWLVSYSPALHPSISEERKYIEDAIGESAKLMNPLTKSTPMRRPFT 300
DB 241 YGSFGIFWYLFMWLVSYSPALHPSISEERKYIEDAIGESAKLMNPLTKSTPMRRPFT 300
QY 301 SMPVYAIIVANPCSWMTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWMTIIVPIGQ 360
DB 301 SMPVYAIIVANPCSWMTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWMTIIVPIGQ 360
QY 361 IADFLRSRIMSTNVKRLMNCGFGMEATLLVVGYSKGAIVISFLVAVGSGFAIS 420
DB 361 IADFLRSRIMSTNVKRLMNCGFGMEATLLVVGYSKGAIVISFLVAVGSGFAIS 420
QY 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREMOYVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREMOYVFLIASLVHY 480
QY 481 GGVIFYGVFASGEKQPMAPPEMSEKCGFVGHDLASDSEMEDAEPPGAPPAPPS 540
DB 481 GGVIFYGVFASGEKQPMAPPEMSEKCGFVGHDLASDSEMEDAEPPGAPPAPPS 540
QY 541 YGATHSTQPPRPVVDY 560
DB 541 YGATHSTQPPRPVVDY 560
  
```

RESULT 4
 PCT-US98-02875-5
 Sequence 5, Application PC/TUS9802875
 GENERAL INFORMATION:
 APPLICANT: EMORY UNIVERSITY
 APPLICANT: Gunn, Robert B.
 APPLICANT: Timmer, Richard T.
 TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
 TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kildpatrick Stockton LLP
 STREET: Suite 2800, 1100 Peachtree Street NE
 CITY: Atlanta
 STATE: GA
 COUNTRY: USA
 ZIP: 30309-4530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US98/02875
 FILING DATE: 11-FEB-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/039,462
 FILING DATE: 7-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Meredith, Roy D.
 REGISTRATION NUMBER: 30,777
 REFERENCE/DOCKET NUMBER: EMU13PCT
 TELEPHONE: (404) 815-6500
 TELEFAX: (404) 815-6555
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 560 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHEICAL: NO
 FRAGMENT TYPE: N-terminal
 FEATURE:
 NAME/KEY: hBNPI
 LOCATION: 1..560
 PUBLICATION INFORMATION:
 DOCUMENT NUMBER: Ni, B., et al.,
 DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)
 PCT-US98-02875-5

Query Match 99.9%; Score 2967; DB 1; Length 560;
 Best Local Similarity 99.8%; Pred. No. 3.5e-272;
 Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MEFROEERKLAGRALGKHLRLERKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERKLAGRALGKHLRLERKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAINGSGFCISFGIRCNLGAIVSMVNNSTTHRGHVVOKAFSMDPETVGLIH 120
DB 61 RRYIIAINGSGFCISFGIRCNLGAIVSMVNNSTTHRGHVVOKAFSMDPETVGLIH 120
QY 121 GSFPMGYIVTOIPGSGFCOKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRIIOG 180
DB 121 GSFPMGYIVTOIPGSGFCOKFAANRVFGFAIVATSTLMLIPSAARVHYGCVIFVRIIOG 180
QY 181 LVEGTVYACGIGMSKMAPLERSLATTAFCGSYAGAVVAMPAGLVVOYSGMSSVRYV 240
DB 181 LVEGTVYACGIGMSKMAPLERSLATTAFCGSYAGAVVAMPAGLVVOYSGMSSVRYV 240
QY 241 YGSFGIFWYLFMWLVSYSPALHPSISEERKYIEDAIGESAKLMNPLTKSTPMRRPFT 300
DB 241 YGSFGIFWYLFMWLVSYSPALHPSISEERKYIEDAIGESAKLMNPLTKSTPMRRPFT 300
QY 301 SMPVYAIIVANPCSWMTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWMTIIVPIGQ 360
DB 301 SMPVYAIIVANPCSWMTFYLLISQPDYFEEVFGFELSKVGLVSLPHLWMTIIVPIGQ 360
QY 361 IADFLRSRIMSTNVKRLMNCGFGMEATLLVVGYSKGAIVISFLVAVGSGFAIS 420
DB 361 IADFLRSRIMSTNVKRLMNCGFGMEATLLVVGYSKGAIVISFLVAVGSGFAIS 420
QY 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREMOYVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHKTREMOYVFLIASLVHY 480
  
```

QY 481 GGVIYGVASGEKOPMAPEEMSEKCGFYVGHDLASGSDSEMEDEAPPGAPAPPPS 540
DB 481 GGVIYGVASGEKOPMAPEEMSEKCGFYVGHDLASGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATSTFOPRPPRPVPRDY 560
DB 541 YGATSTFOPRPPRPVPRDY 560

RESULT 5
PCT-US98-02875A-5
Sequence 5, Application PC/TUS9802875A
GENERAL INFORMATION:
APPLICANT: EMORY UNIVERSITY
APPLICANT: Gunn, Robert B.
APPLICANT: Timmer, Richard T.
TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kildpatrick Stockton LLP
STREET: Suite 2800, 1100 Peachtree Street NE
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02875A
FILING DATE: 11-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,462
FILING DATE: 27-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: EM0153PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6550
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: hBNP1
LOCATION: 1..560
PUBLICATION INFORMATION:
DOCUMENT NUMBER: NI, B., et al.,
DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)
PCT-US98-02875A-5

Query Match 99.9%; Score 2967; DB 1; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFRQEEFKLAGRAFGKLRLEKROGAETLELSADRPVYTTOTRDPVPVVDCTCFGLP 60
DB 1 MEFRQEEFKLAGRAFGKLRLEKROGAETLELSADRPVYTTOTRDPVPVVDCTCFGLP 60
QY 61 RRYIAINSGLCFCISFGIRCMGVAIVSMVNNSTTHRGHVYVOKAQSMDPETVGLIH 120

DB 61 RRYIAINSGLCFCISFGIRCMGVAIVSMVNNSTTHRGHVYVOKAQSMDPETVGLIH 120
QY 121 GSFPMGYIVTQIPGGFICQKPAANVPFGPAIVATSTLMLIPSAARVHYGCVIFVRIIQQ 180
DB 121 GSFPMGYIVTQIPGGFICQKPAANVPFGPAIVATSTLMLIPSAARVHYGCVIFVRIIQQ 180
QY 181 LVEGVTYPACGHWKMAPELERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
DB 181 LVEGVTYPACGHWKMAPELERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
QY 241 YSGFIFWYLFVILVSYSPALHPISISEERKIIDALIGESAKLNPITKSTPMRRPFT 300
DB 241 YSGFIFWYLFVILVSYSPALHPISISEERKIIDALIGESAKLNPITKSTPMRRPFT 300
QY 301 SMPVVAIVANFCRSWTFYLLIISQPDYFEEVFGFEISKVGIVSALPHLWMTIIVPISGQ 360
DB 301 SMPVVAIVANFCRSWTFYLLIISQPDYFEEVFGFEISKVGIVSALPHLWMTIIVPISGQ 360
QY 361 IADFLRSRINSTNVRKLMNCGFGFMEATILLVVGYSKGVASISFLVAVGSGFAIS 420
DB 361 IADFLRSRINSTNVRKLMNCGFGFMEATILLVVGYSKGVASISFLVAVGSGFAIS 420
QY 421 GPNVHLLIAPRYASILNGISNGVTLGMCPIIVGAMTKHKTREEMQYVFLASLVHY 480
DB 421 GPNVHLLIAPRYASILNGISNGVTLGMCPIIVGAMTKHKTREEMQYVFLASLVHY 480
QY 481 GGVIYGVASGEKOPMAPEEMSEKCGFYVGHDLASGSDSEMEDEAPPGAPAPPPS 540
DB 481 GGVIYGVASGEKOPMAPEEMSEKCGFYVGHDLASGSDSEMEDEAPPGAPAPPPS 540
QY 541 YGATSTFOPRPPRPVPRDY 560
DB 541 YGATSTFOPRPPRPVPRDY 560

RESULT 6
US-09-380-164-5
Sequence 5, Application US/09380164
GENERAL INFORMATION:
APPLICANT: EMORY UNIVERSITY
APPLICANT: Gunn, Robert B.
APPLICANT: Timmer, Richard T.
TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kildpatrick Stockton LLP
STREET: Suite 2800, 1100 Peachtree Street NE
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,164
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/02875
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: EM0153PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6550
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:

LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: hbnp1
LOCATION: 1..560
PUBLICATION INFORMATION:
DOCUMENT NUMBER: N1, B., et al.,
DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)
US-09-380-164-5

Query Match 99.9%; Score 2967; DB 17; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFOEERKLAGRLGKRLHLEKROGAETLELSADGRPTTQTRDPVVDCTCGLP 60
DB 1 MEFOEERKLAGRLGKRLHLEKROGAETLELSADGRPTTQTRDPVVDCTCGLP 60
QY 61 RRYIIAISMGLGFCISFGIRCNLGVAVSMVNSSTTRGGHVVOXKQFSDPETVGLIH 120
DB 61 RRYIIAISMGLGFCISFGIRCNLGVAVSMVNSSTTRGGHVVOXKQFSDPETVGLIH 120
QY 121 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMNLIPSARVHYGCVIFVRILQG 180
DB 121 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMNLIPSARVHYGCVIFVRILQG 180
QY 181 LVEGVTYPACHGINSKMAPPLERSRLATTACGSYAGAVVAMPPLAGVLVOYSGMSVFYV 240
DB 181 LVEGVTYPACHGINSKMAPPLERSRLATTACGSYAGAVVAMPPLAGVLVOYSGMSVFYV 240
QY 241 YGSGFIFMYLFWLVSYPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPMRRPFT 300
DB 241 YGSGFIFMYLFWLVSYPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPMRRPFT 300
QY 301 SMPYVAIIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVGLVSALPHLVNTIIVPIGQ 360
DB 301 SMPYVAIIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVGLVSALPHLVNTIIVPIGQ 360
QY 361 IADFLRSRIMSTTNVRKLNCCGFGMEATLLLVGYSKGVASIFVLAVGSGFAIS 420
DB 361 IADFLRSRIMSTTNVRKLNCCGFGMEATLLLVGYSKGVASIFVLAVGSGFAIS 420
QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGWCPIIVGAMTKHKTREMOYVFLASLVHY 480
DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGWCPIIVGAMTKHKTREMOYVFLASLVHY 480
QY 481 GGVIFYGVFASGEKQPAPEPEMSEKCGFYGHQDLAGSDSEMEDAEPGAPAPAPPS 540
DB 481 GGVIFYGVFASGEKQPAPEPEMSEKCGFYGHQDLAGSDSEMEDAEPGAPAPAPPS 540
QY 541 YGATHSTFQPPRPVVDY 560
DB 541 YGATHSTFQPPRPVVDY 560

RESULT 7
US-10-314-790-5
GENERAL INFORMATION:
APPLICANT: EMORY UNIVERSITY
Gunn, Robert B.
Timmer, Richard T.
TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Kilpatrick Stockton LLP
STREET: Suite 2800, 1100 Peachtree Street NE

CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/314,790
FILING DATE: 09-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/380,164
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US98/02875
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meredith, Roy D.
REGISTRATION NUMBER: 30,777
REFERENCE/DOCKET NUMBER: EM0153PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6500
TELEFAX: (404) 815-6555
SEQUENCE DESCRIPTION: SEQ ID NO: 5
US-10-314-790-5

Query Match 99.9%; Score 2967; DB 29; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFOEERKLAGRLGKRLHLEKROGAETLELSADGRPTTQTRDPVVDCTCGLP 60
DB 1 MEFOEERKLAGRLGKRLHLEKROGAETLELSADGRPTTQTRDPVVDCTCGLP 60
QY 61 RRYIIAISMGLGFCISFGIRCNLGVAVSMVNSSTTRGGHVVOXKQFSDPETVGLIH 120
DB 61 RRYIIAISMGLGFCISFGIRCNLGVAVSMVNSSTTRGGHVVOXKQFSDPETVGLIH 120
QY 121 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMNLIPSARVHYGCVIFVRILQG 180
DB 121 GSPFMGYIVTQIPGGFICQKFAANRVFGFAIVATSTLMNLIPSARVHYGCVIFVRILQG 180
QY 181 LVEGVTYPACHGINSKMAPPLERSRLATTACGSYAGAVVAMPPLAGVLVOYSGMSVFYV 240
DB 181 LVEGVTYPACHGINSKMAPPLERSRLATTACGSYAGAVVAMPPLAGVLVOYSGMSVFYV 240
QY 241 YGSGFIFMYLFWLVSYPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPMRRPFT 300
DB 241 YGSGFIFMYLFWLVSYPALHPSISEEERKYIEDAIGESAKLMNPLTKFSTPMRRPFT 300
QY 301 SMPYVAIIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVGLVSALPHLVNTIIVPIGQ 360
DB 301 SMPYVAIIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVGLVSALPHLVNTIIVPIGQ 360
QY 361 IADFLRSRIMSTTNVRKLNCCGFGMEATLLLVGYSKGVASIFVLAVGSGFAIS 420
DB 361 IADFLRSRIMSTTNVRKLNCCGFGMEATLLLVGYSKGVASIFVLAVGSGFAIS 420
QY 421 GFNNHLDIAPRYASILMGISNGVGTLSGWCPIIVGAMTKHKTREMOYVFLASLVHY 480
DB 421 GFNNHLDIAPRYASILMGISNGVGTLSGWCPIIVGAMTKHKTREMOYVFLASLVHY 480
QY 481 GGVIFYGVFASGEKQPAPEPEMSEKCGFYGHQDLAGSDSEMEDAEPGAPAPAPPS 540
DB 481 GGVIFYGVFASGEKQPAPEPEMSEKCGFYGHQDLAGSDSEMEDAEPGAPAPAPPS 540
QY 541 YGATHSTFQPPRPVVDY 560
DB 541 YGATHSTFQPPRPVVDY 560

```
RESULT 8
US-60-039-462-5
; Sequence 5, Application US/60039462
; GENERAL INFORMATION:
; APPLICANT: Gunn, Robert B.
; TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN
; TITLE OF INVENTION: LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick Stockton LLP
; STREET: Suite 2800, 1100 Peachtree Street NE
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/60/039,462
; FILING DATE: 27-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Meredith, Roy D.
; REGISTRATION NUMBER: 30,777
; REFERENCE/DOCKET NUMBER: E269/99809-EMU153
; TELEPHONE: (404) 815-6500
; TELEFAX: (404) 815-6555
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: hbnpt
; LOCATION: 1..560
; PUBLICATION INFORMATION:
; DOCUMENT NUMBER: N1, B, et al.
; DOCUMENT NUMBER: J. Neurochem., 66:2227 (1996)
; US-60-039-462-5

Query Match          99.9%; Score 2967; DB 37; Length 560;
Best Local Similarity 99.8%; Pred. No. 3.5e-272;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFROEERFKLAGRALGKHLRLLEKROGAEETLEISADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERFKLAGRALGKHLRLLEKROGAEETLEISADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOXKQFSMDPEVGLIH 120
DB 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOXKQFSMDPEVGLIH 120
QY 121 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
DB 121 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
QY 122 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
DB 122 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
QY 181 LVEGVTPACHGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
DB 181 LVEGVTPACHGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
QY 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
DB 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
QY 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
DB 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
```

```
QY 301 SMPVYAIIVANFCRSWTFYLLISOPDYFEEVFGFEISKVGLVSLPHIWMITIVPIGQ 360
DB 301 SMPVYAIIVANFCRSWTFYLLISOPDYFEEVFGFEISKVGLVSLPHIWMITIVPIGQ 360
QY 361 IADFLRSRIMSTNVKRLKMGCGFMEATLLLVGYSHSKVAISFLVLAANGSGFAIS 420
DB 361 IADFLRSRIMSTNVKRLKMGCGFMEATLLLVGYSHSKVAISFLVLAANGSGFAIS 420
QY 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVFLIASLVHY 480
QY 481 GGVIFVYPASGEKOPMAPEEEMSEKCGFVGHDLAAGSDSEMEDEAPPAAPPAPS 540
DB 481 GGVIFVYPASGEKOPMAPEEEMSEKCGFVGHDLAAGSDSEMEDEAPPAAPPAPS 540
QY 541 YGATHSTQPPRRPPPPVVDY 560
DB 541 YGATHSTQPPRRPPPPVVDY 560

RESULT 9
US-10-170-205E-18690
; Sequence 18690, Application US/10170205E
; GENERAL INFORMATION:
; APPLICANT: ADAMS, Mark
; TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
; TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
; FILE REFERENCE: C1001381
; CURRENT APPLICATION NUMBER: US/10/170,205E
; CURRENT FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 40312
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 18690
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-170-205E-18690

Query Match          99.7%; Score 2962; DB 27; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEFROEERFKLAGRALGKHLRLLEKROGAEETLEISADGRPVTTQTRDPVVDCTCFGLP 60
DB 1 MEFROEERFKLAGRALGKHLRLLEKROGAEETLEISADGRPVTTQTRDPVVDCTCFGLP 60
QY 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOXKQFSMDPEVGLIH 120
DB 61 RRYIIAIMGSGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVVOXKQFSMDPEVGLIH 120
QY 121 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
DB 121 GSEFMGIVTQIPGGFICQKFAANRVFGFAIVATSTLNLIPSAARVHGVCFVRIILOG 180
QY 181 LVEGVTPACHGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
DB 181 LVEGVTPACHGIMSKMAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGMSVFYV 240
QY 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
DB 241 YSFGIFMYLFWLLVYSBPALHPSISEERKYIEDAIGESAKLNNPLTKFSTPMRRPFT 300
QY 301 SMPVYAIIVANFCRSWTFYLLISOPDYFEEVFGFEISKVGLVSLPHIWMITIVPIGQ 360
DB 301 SMPVYAIIVANFCRSWTFYLLISOPDYFEEVFGFEISKVGLVSLPHIWMITIVPIGQ 360
QY 361 IADFLRSRIMSTNVKRLKMGCGFMEATLLLVGYSHSKVAISFLVLAANGSGFAIS 420
DB 361 IADFLRSRIMSTNVKRLKMGCGFMEATLLLVGYSHSKVAISFLVLAANGSGFAIS 420
QY 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGLSGMVCPIIVGAMTKHTEEMQVFLIASLVHY 480
```

```

Db 421 GFNVHLDIARVYASILMGISNGVGTLSGMVCPILVGMATGKTKREEMQVFLIASLVHY 480
Qy 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540
Db 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540
Qy 541 YGATHSTFQPPRPPPPVADY 560
Db 541 YGATHSTFQPPRPPPPVADY 560

RESULT 10
US-10-734-731-2
; Sequence 2, Application US/10734731
; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAFER, MARTIN
; TITLE OF INVENTION: SCREENING METHOD USING BNPI AND DNPI
; FILE REFERENCE: 029310.5295US
; CURRENT APPLICATION NUMBER: US/10/734,731
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: PCT/EP02/06484
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: DE 101 28 541.8
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-734-731-2

```

```

Query Match 99.7%; Score 2962; DB 33; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 MEPRQEEFRKLKAGRLGKHLRLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
Db 1 MEPRQEEFRKLKAGRLGKHLRLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
Qy 61 RRYIIAIMGSGFICISFGIRCNLCVAIVSMVNNSTTHRGHVVOXKQFSDPDTVGLIH 120
Db 61 RRYIIAIMGSGFICISFGIRCNLCVAIVSMVNNSTTHRGHVVOXKQFSDPDTVGLIH 120
Qy 61 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 61 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Db 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Qy 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Db 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Qy 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Db 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Qy 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Db 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Qy 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Db 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Qy 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Db 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Qy 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Db 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Qy 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Db 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Qy 421 GFNVHLDIARVYASILMGISNGVGTLSGMVCPILVGMATGKTKREEMQVFLIASLVHY 480
Db 421 GFNVHLDIARVYASILMGISNGVGTLSGMVCPILVGMATGKTKREEMQVFLIASLVHY 480
Qy 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540
Db 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540

```

```

Qy 541 YGATHSTFQPPRPPPPVADY 560
Db 541 YGATHSTFQPPRPPPPVADY 560

```

```

RESULT 11
US-10-756-149-5598
; Sequence 5598, Application US/10756149
; GENERAL INFORMATION:
; APPLICANT: Aziz, Nataasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; PRIOR FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5598
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5598

```

```

Query Match 99.7%; Score 2962; DB 33; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 MEPRQEEFRKLKAGRLGKHLRLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
Db 1 MEPRQEEFRKLKAGRLGKHLRLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLP 60
Qy 61 RRYIIAIMGSGFICISFGIRCNLCVAIVSMVNNSTTHRGHVVOXKQFSDPDTVGLIH 120
Db 61 RRYIIAIMGSGFICISFGIRCNLCVAIVSMVNNSTTHRGHVVOXKQFSDPDTVGLIH 120
Qy 61 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 61 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Db 121 GSFFMGYIVTQIPGGFICQKFAANRVFGFALVATSTLNMILPSARVHYGCVIFVRILOG 180
Qy 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Db 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Qy 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Db 181 LVEGTYTPACHGIMSKAPPLERSRLATTAFCSYAGAVVAMPPLAGVLVOYSGMSVYV 240
Qy 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Db 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Qy 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Db 241 YGSFGIFWYLFMWLVSYSPALHPSISEBERKYIEDAIGESAKLMNPLTKFSTPWRREF 300
Qy 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Db 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Qy 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Db 301 SMPVYAIIVANFCSWTFYLLISQPDYFEEVFEISKVLVSNALPHLVNTIIVPIGQ 360
Qy 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Db 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Qy 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Db 361 IADFLRSRRIMSTNVKRLKMGCGFGMEATLLLVGYSHSGVAISFLVLAVGSFAIS 420
Qy 421 GFNVHLDIARVYASILMGISNGVGTLSGMVCPILVGMATGKTKREEMQVFLIASLVHY 480
Db 421 GFNVHLDIARVYASILMGISNGVGTLSGMVCPILVGMATGKTKREEMQVFLIASLVHY 480
Qy 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540
Db 481 GGVIIFYGVFASGKQPMABPEEMSEKCGFVGHDLASDSEMEDAEAPPGAPAPPPS 540
Qy 541 YGATHSTFQPPRPPPPVADY 560
Db 541 YGATHSTFQPPRPPPPVADY 560

```

```

RESULT 12
US-10-807-500-2
; Sequence 2, Application US/10807500

```

```

; GENERAL INFORMATION:
; APPLICANT: WEIHE, EBERHARD
; APPLICANT: SCHAEFER, MARTIN
; TITLE OF INVENTION: SCREENING PROCESS FOR VARIOUS INDICATIONS USING BNPI AND/OR DNPI
; FILE REFERENCE: 029310.53352US
; CURRENT APPLICATION NUMBER: US/10/807,500
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: PCT/EP02/10707
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 006.1
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: DE 101 47 028.2
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-807-500-2

```

```

Query Match          99.7%; Score 2962; DB 34; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 MEPRQEEPRKLAGRALGKLRLLLEKROEGAEITLISADGRPVTTQTRDPVPVDDCTCFGLP 60
DB      1 MEPRQEEPRKLAGRALGKLRLLLEKROEGAEITLISADGRPVTTQTRDPVPVDDCTCFGLP 60
QY      61 RRYIIAIMGSLGFCISFGIRCNIGVAIVSMVNNSTTHRGHVVOKAQFSMDPETVGLIH 120
DB      61 RRYIIAIMGSLGFCISFGIRCNIGVAIVSMVNNSTTHRGHVVOKAQFSMDPETVGLIH 120
QY      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
DB      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
QY      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
DB      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
QY      181 LVEGVTPACHGIMSKMAPLERSLATTAFGSGYAGAVVAMPVLAVGVQSGMSVFFV 240
DB      181 LVEGVTPACHGIMSKMAPLERSLATTAFGSGYAGAVVAMPVLAVGVQSGMSVFFV 240
QY      241 YGSFGIFWTLFWLTVSYESPALHPSISEBERKTIIDAIAGESAKLNPLTKFSTPMRRPFT 300
DB      241 YGSFGIFWTLFWLTVSYESPALHPSISEBERKTIIDAIAGESAKLNPLTKFSTPMRRPFT 300
QY      301 SMPVVAIIYANCRSWTFYLLISQPDYFEEVGFGEISKVGLVSALPHLWMTIIVPIGQ 360
DB      301 SMPVVAIIYANCRSWTFYLLISQPDYFEEVGFGEISKVGLVSALPHLWMTIIVPIGQ 360
QY      361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGSGFAIS 420
DB      361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGSGFAIS 420
QY      421 GENVNHLDIAPRYASILMGSINGVGLSGMVCPIIVGAMTKKTKREMOYVFLIASLVHY 480
DB      421 GENVNHLDIAPRYASILMGSINGVGLSGMVCPIIVGAMTKKTKREMOYVFLIASLVHY 480
QY      481 GGVIIFYGVFASGEKOPMAEPBEEMSEKCGFVGHDLAGSDSEMEDEAPPGAPAPPPS 540
DB      481 GGVIIFYGVFASGEKOPMAEPBEEMSEKCGFVGHDLAGSDSEMEDEAPPGAPAPPPS 540
QY      541 YGATHSTFQPPRPPPPVVDY 560
DB      541 YGATHSTFQPPRPPPPVVDY 560

```

```

RESULT 13
US-60-452-680-12892
; Sequence 12892, Application US/60452680
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: GRUBE, Andrew
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

```

```

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001450
; CURRENT APPLICATION NUMBER: US/60/452,680
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 116213
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12892
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-452-680-12892

```

```

Query Match          99.7%; Score 2962; DB 37; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 MEPRQEEPRKLAGRALGKLRLLLEKROEGAEITLISADGRPVTTQTRDPVPVDDCTCFGLP 60
DB      1 MEPRQEEPRKLAGRALGKLRLLLEKROEGAEITLISADGRPVTTQTRDPVPVDDCTCFGLP 60
QY      61 RRYIIAIMGSLGFCISFGIRCNIGVAIVSMVNNSTTHRGHVVOKAQFSMDPETVGLIH 120
DB      61 RRYIIAIMGSLGFCISFGIRCNIGVAIVSMVNNSTTHRGHVVOKAQFSMDPETVGLIH 120
QY      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
DB      121 GSEFWGYITQIPGGFICQKFAANRVFGPAIVATSTLNLIPSAARVHYGCVIFVRILOG 180
QY      181 LVEGVTPACHGIMSKMAPLERSLATTAFGSGYAGAVVAMPVLAVGVQSGMSVFFV 240
DB      181 LVEGVTPACHGIMSKMAPLERSLATTAFGSGYAGAVVAMPVLAVGVQSGMSVFFV 240
QY      241 YGSFGIFWTLFWLTVSYESPALHPSISEBERKTIIDAIAGESAKLNPLTKFSTPMRRPFT 300
DB      241 YGSFGIFWTLFWLTVSYESPALHPSISEBERKTIIDAIAGESAKLNPLTKFSTPMRRPFT 300
QY      301 SMPVVAIIYANCRSWTFYLLISQPDYFEEVGFGEISKVGLVSALPHLWMTIIVPIGQ 360
DB      301 SMPVVAIIYANCRSWTFYLLISQPDYFEEVGFGEISKVGLVSALPHLWMTIIVPIGQ 360
QY      361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGSGFAIS 420
DB      361 IADFLRSRIMSTTVNRKLMNCGFGMEATLLLVGYSHSKGVAISFLVLAVGSGFAIS 420
QY      421 GENVNHLDIAPRYASILMGSINGVGLSGMVCPIIVGAMTKKTKREMOYVFLIASLVHY 480
DB      421 GENVNHLDIAPRYASILMGSINGVGLSGMVCPIIVGAMTKKTKREMOYVFLIASLVHY 480
QY      481 GGVIIFYGVFASGEKOPMAEPBEEMSEKCGFVGHDLAGSDSEMEDEAPPGAPAPPPS 540
DB      481 GGVIIFYGVFASGEKOPMAEPBEEMSEKCGFVGHDLAGSDSEMEDEAPPGAPAPPPS 540
QY      541 YGATHSTFQPPRPPPPVVDY 560
DB      541 YGATHSTFQPPRPPPPVVDY 560

```

```

RESULT 14
US-60-453-050-8103
; Sequence 8103, Application US/60453050
; GENERAL INFORMATION:
; APPLICANT: LUKE, May
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001457
; CURRENT APPLICATION NUMBER: US/60/453,050
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8103
; LENGTH: 560
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-60-453-050-8103

Query Match      99.7%; Score 2962; DB 37; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEFRQEEFRKLGRALGKHLRLLEKROGAEATLELSADGRPVTTQTDRPPVVDCTCFGLP 60
Db |
Qy 1 MEFRQEEFRKLGRALGKHLRLLEKROGAEATLELSADGRPVTTQTDRPPVVDCTCFGLP 60
Db |
Qy 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVIVSMVNNSTTHRGHVVVQKQAFSMDPETVGLIH 120
Db |
Qy 121 GSFFWGIIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db |
Qy 181 LVEGVTPACHGKWSKAPPLERSRLATTAPCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Db |
Qy 241 YGSFGIFWYLFWLLVSVESPALHPSISEERKYIEDAIGESAKLMNPLTKFSTPWRPFT 300
Db |
Qy 301 SMPVYAIIVANFCRSWTFYLLLIISQPDYFEEVGFGEISKVGLVLSALPHLVNTIIVPIGGQ 360
Db |
Qy 361 IADFLRRRIMSTTNVRKLMNCGFGMEATLLLVVGYSHSGVAISFLVLAVGSGFAIS 420
Db |
Qy 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVHY 480
Db |
Qy 481 GGVIYGVFASGEKQWAEPEEMSEKCGFVGHDLQAGSDDEDAEPPGAPPAPPPS 540
Db |
Qy 541 YGATHSTFQPPRPPPPVRDY 560
Db |
Qy 541 YGATHSTFQPPRPPPPVRDY 560
Db |

RESULT 15
US-60-453-135-8103
; Sequence 8103, Application US/60453135
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; APPLICANT: IAKOUBOVA, Olga
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001456
; CURRENT APPLICATION NUMBER: US/60/453,135
; CURRENT FILING DATE: 2003-03-10
; NUMBER OF SEQ ID NOS: 82762
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8103
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-453-135-8103

Query Match      99.7%; Score 2962; DB 37; Length 560;
Best Local Similarity 99.8%; Pred. No. 1e-271;
Matches 559; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEFRQEEFRKLGRALGKHLRLLEKROGAEATLELSADGRPVTTQTDRPPVVDCTCFGLP 60
Db |

```

```

Db 1 MEFRQEEFRKLGRALGKHLRLLEKROGAEATLELSADGRPVTTQTDRPPVVDCTCFGLP 60
Qy 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVIVSMVNNSTTHRGHVVVQKQAFSMDPETVGLIH 120
Db 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVIVSMVNNSTTHRGHVVVQKQAFSMDPETVGLIH 120
Qy 121 GSFFWGIIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db 121 GSFFWGIIVTQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Qy 181 LVEGVTPACHGKWSKAPPLERSRLATTAPCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Db 181 LVEGVTPACHGKWSKAPPLERSRLATTAPCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
Qy 241 YGSFGIFWYLFWLLVSVESPALHPSISEERKYIEDAIGESAKLMNPLTKFSTPWRPFT 300
Db 241 YGSFGIFWYLFWLLVSVESPALHPSISEERKYIEDAIGESAKLMNPLTKFSTPWRPFT 300
Qy 301 SMPVYAIIVANFCRSWTFYLLLIISQPDYFEEVGFGEISKVGLVLSALPHLVNTIIVPIGGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLLIISQPDYFEEVGFGEISKVGLVLSALPHLVNTIIVPIGGQ 360
Qy 361 IADFLRRRIMSTTNVRKLMNCGFGMEATLLLVVGYSHSGVAISFLVLAVGSGFAIS 420
Db 361 IADFLRRRIMSTTNVRKLMNCGFGMEATLLLVVGYSHSGVAISFLVLAVGSGFAIS 420
Qy 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVHY 480
Db 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVHY 480
Qy 481 GGVIYGVFASGEKQWAEPEEMSEKCGFVGHDLQAGSDDEDAEPPGAPPAPPPS 540
Db 481 GGVIYGVFASGEKQWAEPEEMSEKCGFVGHDLQAGSDDEDAEPPGAPPAPPPS 540
Qy 541 YGATHSTFQPPRPPPPVRDY 560
Db 541 YGATHSTFQPPRPPPPVRDY 560

```

Search completed: June 2, 2005, 11:41:01
Job time : 481 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 11:31:49 ; Search time 140 Seconds
(without alignments)
1382.720 Million cell updates/sec

Title: US-10-734-731-4

Perfect score: 2970

Sequence: 1 MFRQBEERKLGRALGKUH.....YGATHSTFQPRPPPPVRDY 560

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 1465611

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2967	99.9	560	15	US-10-314-790-5
2	2925	98.5	560	9	US-09-991-212A-4
3	2925	98.5	560	9	US-09-915-181A-5
4	2925	98.5	560	10	US-09-965-522-4
5	2925	98.5	560	17	US-10-877-818-4
6	2313.5	77.9	578	9	US-09-740-041-4
7	2313.5	77.9	578	14	US-10-389-967-4
8	2313.5	77.9	578	4	US-09-915-181A-4
9	2313.5	77.9	582	15	US-10-205-331-7
10	2185	73.6	589	9	US-09-740-041-2
11	2185	73.6	589	14	US-10-389-967-2
12	2174.5	73.2	850	9	US-09-915-181A-3
13	2138.5	72.0	566	15	US-10-287-226-300

14	1297	43.7	576	14	US-10-014-079A-1	Sequence 1, Appli
15	1297	43.7	576	15	US-10-369-493-5823	Sequence 5823, Ap
16	1294	43.6	563	9	US-09-915-181A-6	Sequence 6, Appli
17	1186	39.9	264	15	US-10-108-260A-3281	Sequence 3281, Ap
18	1025.5	34.5	204	15	US-10-104-047-2253	Sequence 2253, Ap
19	971	32.7	573	15	US-10-369-493-5871	Sequence 5871, Ap
20	971	32.7	573	15	US-10-369-493-5872	Sequence 5872, Ap
21	950	32.0	544	15	US-10-369-493-5873	Sequence 5873, Ap
22	940	31.6	495	9	US-09-915-181A-7	Sequence 7, Appli
23	940	31.6	495	16	US-10-755-889-588	Sequence 588, App
24	940	31.6	495	16	US-10-823-506-2	Sequence 2, Appli
25	940	31.6	536	9	US-09-776-865-2	Sequence 8, Appli
26	940	31.6	536	16	US-10-823-506-8	Sequence 2, Appli
27	931	31.3	495	9	US-09-776-865-4	Sequence 4, Appli
28	931	31.3	495	16	US-10-823-506-4	Sequence 4, Appli
29	775.5	26.1	493	15	US-10-369-493-5834	Sequence 5834, Ap
30	765.5	25.8	662	15	US-10-425-114-67137	Sequence 67137, A
31	734.5	24.7	591	16	US-10-437-963-160214	Sequence 160214, A
32	715.5	24.1	470	16	US-10-767-701-44234	Sequence 44234, A
33	709	23.9	513	15	US-10-424-599-149883	Sequence 149883, A
34	636.5	21.4	495	16	US-10-823-506-10	Sequence 10, Appl
35	636.5	21.4	495	16	US-10-823-506-12	Sequence 12, Appl
36	626.5	21.1	467	9	US-09-991-212A-3	Sequence 3, Appli
37	626.5	21.1	467	10	US-09-965-522-3	Sequence 3, Appli
38	615	20.7	465	9	US-09-915-181A-8	Sequence 8, Appli
39	615	20.7	465	15	US-10-425-114-64466	Sequence 64466, A
40	576	19.4	445	15	US-10-264-049-2477	Sequence 2477, Ap
41	561	18.9	284	16	US-10-437-963-180313	Sequence 180313, A
42	555.5	18.7	428	16	US-10-264-237-2351	Sequence 2351, Ap
43	530	17.8	272	15	US-10-425-114-47324	Sequence 47324, A
44	489	16.5	283	15	US-10-424-599-279212	Sequence 279212, A
45	488.5	16.4	449	15	US-10-424-599-279212	Sequence 279212, A

ALIGNMENTS

RESULT 1

US-10-314-790-5

GENERAL APPLICANT: EMORY UNIVERSITY

Gunn, Robert B.

Timmer, Richard T.

TITLE OF INVENTION: SODIUM-PHOSPHATE COTRANSPORTER IN

LITHIUM THERAPY FOR THE TREATMENT OF MENTAL ILLNESS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kilpatrick Stockton LLP

STREET: Suite 2800, 1100 Peachtree Street NE

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-4530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/314,790

FILING DATE: 09-Dec-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/380,164

FILING DATE: <Unknown>

APPLICATION NUMBER: PCT/US98/02875

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Meredith, Roy D.

REGISTRATION NUMBER: 30,777

REFERENCE/DOCKET NUMBER: EMU153PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 815-6500

TELEFAX: (404) 815-6555
SEQUENCE DESCRIPTION: SEQ ID NO: 5;
US-10-314-790-5

Query Match 99.9%; Score 2967; DB 15; Length 560;
Best Local Similarity 99.8%; Pred. No. 2.7e-258;
Matches 559; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEFRQEEPRKLAGALGKHLRLEKQGAETLELSADGRPVTTOTRPPVVDCTCFGLP 60
DB 1 MEFRQEEPRKLAGALGKHLRLEKQGAETLELSADGRPVTTOTRPPVVDCTCFGLP 60

QY 61 RRYIIAIIAMSGLFCISFGIRCNLGVAIIVSMVNNSTTHRGHHVVKQAFSMDPETVGLIH 120
DB 61 RRYIIAIIAMSGLFCISFGIRCNLGVAIIVSMVNNSTTHRGHHVVKQAFSMDPETVGLIH 120

QY 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
DB 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

QY 181 LVEGVYTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
DB 181 LVEGVYTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

QY 241 YGSFGIFWYLFWLLVSVSPALHPSISEERKYIEDAIGESAKLMNPLTKFTPWRRPFT 300
DB 241 YGSFGIFWYLFWLLVSVSPALHPSISEERKYIEDAIGESAKLMNPLTKFTPWRRPFT 300

QY 301 SMPVYAIIVANFCRSWTFFYLLISQPDYFEEVFGFEISKVGLVSALPHLWMTIIVPIGGQ 360
DB 301 SMPVYAIIVANFCRSWTFFYLLISQPDYFEEVFGFEISKVGLVSALPHLWMTIIVPIGGQ 360

QY 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSGVAISFLVLAVGFGSPAIS 420
DB 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSGVAISFLVLAVGFGSPAIS 420

QY 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHY 480

QY 481 GGVIFYGVFASGEKQPWAEPEEMSEKCGFVGHDLQAGSDDEMEDEAEPPGAPPAPPPS 540
DB 481 GGVIFYGVFASGEKQPWAEPEEMSEKCGFVGHDLQAGSDDEMEDEAEPPGAPPAPPPS 540

QY 541 YGATHSTTQPPRPPPPVRDY 560
DB 541 YGATHSTTQPPRPPPPVRDY 560

RESULT 2
US-09-991-212A-4
Sequence 4, Application US/09991212A
Patent No. US20020090691A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/991,212A

Query Match 98.5%; Score 2925; DB 9; Length 560;
Best Local Similarity 98.2%; Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 MEFRQEEPRKLAGALGKHLRLEKQGAETLELSADGRPVTTOTRPPVVDCTCFGLP 60
DB 1 MEFRQEEPRKLAGALGKHLRLEKQGAETLELSADGRPVTTOTRPPVVDCTCFGLP 60

QY 61 RRYIIAIIAMSGLFCISFGIRCNLGVAIIVSMVNNSTTHRGHHVVKQAFSMDPETVGLIH 120
DB 61 RRYIIAIIAMSGLFCISFGIRCNLGVAIIVSMVNNSTTHRGHHVVKQAFSMDPETVGLIH 120

QY 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
DB 121 GSFFWGYIVTQIPGGFICQKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180

QY 181 LVEGVYTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240
DB 181 LVEGVYTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYSGWSSVFYV 240

QY 241 YGSFGIFWYLFWLLVSVSPALHPSISEERKYIEDAIGESAKLMNPLTKFTPWRRPFT 300
DB 241 YGSFGIFWYLFWLLVSVSPALHPSISEERKYIEDAIGESAKLMNPLTKFTPWRRPFT 300

QY 301 SMPVYAIIVANFCRSWTFFYLLISQPDYFEEVFGFEISKVGLVSALPHLWMTIIVPIGGQ 360
DB 301 SMPVYAIIVANFCRSWTFFYLLISQPDYFEEVFGFEISKVGLVSALPHLWMTIIVPIGGQ 360

QY 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSGVAISFLVLAVGFGSPAIS 420
DB 361 IADFLRSRRIMSTTNVRKLMNCGGFGMEATLLLVGYSHSGVAISFLVLAVGFGSPAIS 420

QY 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHY 480
DB 421 GFNVNHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHY 480

QY 481 GGVIFYGVFASGEKQPWAEPEEMSEKCGFVGHDLQAGSDDEMEDEAEPPGAPPAPPPS 540
DB 481 GGVIFYGVFASGEKQPWAEPEEMSEKCGFVGHDLQAGSDDEMEDEAEPPGAPPAPPPS 540

QY 541 YGATHSTTQPPRPPPPVRDY 560
DB 541 YGATHSTTQPPRPPPPVRDY 560

RESULT 3
US-09-915-181A-5
Sequence 5, Application US/09915181A
Patent No. US20020098473A1

GENERAL INFORMATION:
APPLICANT: EDWARDS, ROBERT
APPLICANT: BELLOCCHIO, ELIZABETH
APPLICANT: FREMEAU, ROBERT
APPLICANT: REIMER, RICHARD
TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
FILE REFERENCE: 305T-932610US
CURRENT APPLICATION NUMBER: US/09/915,181A
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/220,556
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 560
TYPE: PRT
ORGANISM: Rattus rattus
US-09-915-181A-5

Query Match 98.5%; Score 2925; DB 9; Length 560;
Best Local Similarity 98.2%; Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEFQEEFRKLKAGLRLHLLKQEGATLELSADGRPVTTQTDRPPVWDCFCGLP 60
Db 1 MEFQEEFRKLKAGLRLHLLKQEGATLELSADGRPVTTHTDRPPVWDCFCGLP 60
Qy 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVSMVNNSTTHRGHVVQKAFQFNDPVTGLIH 120
Db 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVSMVNNSTTHRGHVVQKAFQFNDPVTGLIH 120
Qy 121 GSPFWGVYVITQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db 121 GSPFWGVYVITQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Qy 181 LVEGVYTPACHGIWSKAPPLERSRLATTAPCGSYAGAVVAMPVLAGVLYVQSGWSSVFYV 240
Db 181 LVEGVYTPACHGIWSKAPPLERSRLATTAPCGSYAGAVVAMPVLAGVLYVQSGWSSVFYV 240
Qy 241 YGSFGIFWYLFVLLVSVESPALHPSISEERKYIEDAIGSAKLMNPVTKFPTWRRPFT 300
Db 241 YGSFGIFWYLFVLLVSVESPALHPSISEERKYIEDAIGSAKLMNPVTKFPTWRRPFT 300
Qy 301 SMPVYAIIVANFCRSWTFYLLISQPAYFEVFGFEISKVGLVNSALPHLVMTIIVPIGGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLISQPAYFEVFGFEISKVGLVNSALPHLVMTIIVPIGGQ 360
Qy 361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLVVGYSKGVASIFLVAVGFSGPAIS 420
Db 361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLVVGYSKGVASIFLVAVGFSGPAIS 420
Qy 421 GFNVNHLDIAPRYASILMGISNGVTLSGMVCPPIIVGAMTKHKTRBQVYFLIASLVHY 480
Db 421 GFNVNHLDIAPRYASILMGISNGVTLSGMVCPPIIVGAMTKHKTRBQVYFLIASLVHY 480
Qy 481 GGVIFYGVASGEKQVWAEPEEMSEKCGFVGHDLQAGSDDEMEAEPPGAPPAPPS 540
Db 481 GGVIFYGVASGEKQVWAEPEEMSEKCGFVGHDLQAGSDDEMEAEPPGAPPAPPS 540
Qy 541 YGATHSTVQPPRPPPPVRDY 560
Db 541 YGATHSTVQPPRPPPPVRDY 560

RESULT 4
US-09-965-522-4
Sequence 4, Application US/09965522
Publication No. US20030022325A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
PHOSPHATE CO-TRANSPORTER

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,522
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/391,958
FILING DATE: 1999-09-08
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0221 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 507415
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-965-522-4

Query Match 98.5%; Score 2925; DB 10; Length 560;
Best Local Similarity 98.2%; Pred. No. 1.7e-254;
Matches 550; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEFQEEFRKLKAGLRLHLLKQEGATLELSADGRPVTTQTDRPPVWDCFCGLP 60
Db 1 MEFQEEFRKLKAGLRLHLLKQEGATLELSADGRPVTTHTDRPPVWDCFCGLP 60
Qy 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVSMVNNSTTHRGHVVQKAFQFNDPVTGLIH 120
Db 61 RRYIIAIIAMSGLGFICISFGIRCNLGVAVSMVNNSTTHRGHVVQKAFQFNDPVTGLIH 120
Qy 121 GSPFWGVYVITQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Db 121 GSPFWGVYVITQIPGGFICQKFAANRVGFAIVATSTLNMLIPSAARVHYGCVIFVRILQG 180
Qy 181 LVEGVYTPACHGIWSKAPPLERSRLATTAPCGSYAGAVVAMPVLAGVLYVQSGWSSVFYV 240
Db 181 LVEGVYTPACHGIWSKAPPLERSRLATTAPCGSYAGAVVAMPVLAGVLYVQSGWSSVFYV 240
Qy 241 YGSFGIFWYLFVLLVSVESPALHPSISEERKYIEDAIGSAKLMNPVTKFPTWRRPFT 300
Db 241 YGSFGIFWYLFVLLVSVESPALHPSISEERKYIEDAIGSAKLMNPVTKFPTWRRPFT 300
Qy 301 SMPVYAIIVANFCRSWTFYLLISQPAYFEVFGFEISKVGLVNSALPHLVMTIIVPIGGQ 360
Db 301 SMPVYAIIVANFCRSWTFYLLISQPAYFEVFGFEISKVGLVNSALPHLVMTIIVPIGGQ 360
Qy 361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLVVGYSKGVASIFLVAVGFSGPAIS 420
Db 361 IADFLRSRRIMSTTNVRKLMNCGFGMEATLLVVGYSKGVASIFLVAVGFSGPAIS 420
Qy 421 GFNVNHLDIAPRYASILMGISNGVTLSGMVCPPIIVGAMTKHKTRBQVYFLIASLVHY 480
Db 421 GFNVNHLDIAPRYASILMGISNGVTLSGMVCPPIIVGAMTKHKTRBQVYFLIASLVHY 480


```

; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001-DIV
; CURRENT APPLICATION NUMBER: US/10/389,967
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-389-967-4

Query Match      77.9%; Score 2313.5; DB 14; Length 578;
Best Local Similarity 79.3%; Pred. No. 2.3e-199;
Matches 428; Conservative 57; Mismatches 50; Indels 5; Gaps 2;

Qy 5 QEEPRKLAGRALGKHLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 12 KEGIKNFAGSLGQIYRVLEKKQNRRETIETEDGKPLEVPEKKAPLDCDCTCFGLPRRYI 71
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 65 IAIMSGLGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVQKAFSMDPETHVLIHGSFF 124
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 IAIMSGLGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVQKAFSMDPETHVLIHGSFF 131
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 125 WGYIVTQIPGGFIQCKFAANRVFGFAIVATSTLNLIPSAARVHYGCVIFVRILQGLVEG 184
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 WGYIITQIPGGYIASRLAANRVFGAAILLSTLNLIPSAARVHYGCVIFVRILQGLVEG 191
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 185 VTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPAGVLVQYSGMSSVFVYVGSF 244
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 VTPACHGINSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGILVQYTGWSSVFVYVGSF 251
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 245 GIFWYLFLLVSVESPALHPSISEERKYIEDAIGESAKLNPITKFTSPWRRFFTSMPV 304
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 252 GWMYMFLLVSVESPAKHTITDEERYIEESIGESANLLGAMKEKFTPKRKEFTSMPV 311
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 YAIIVANFCRSWTYLLISOPDYFEEVFGFEISKVGLVLSALPHLVMITIIPIGGQIADF 364
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 YAIIVANFCRSWTYLLISOPDYFEEVFGFEISKVGLVLSALPHLVMITIIPIGGQIADF 371
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 365 LRSRRIMSTTVNRKLMNCGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAISGFNV 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 372 LRSQKILSTTVRKIMNCGFGMEATLLLVVGYSHTRGVASFLVLAVGSGFAISGFNV 431
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 425 NHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHYGGVI 484
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 432 NHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHYGGVI 491
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 485 FYGVFASGEKOPWAEPEEMSEKCGFVGHDLAGSDDEMEDEAEPPCAPPPSYGAT 544
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 492 FYALFASGEKQPWADPEETSEKCGFIHEDEL----DEETGDTIQ-NVINYGTTSYGAT 546

RESULT 8
US-09-915-181A-4
; Sequence 4, Application US/09915181A
; Patent No. US20020098473A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAU, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915,181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11

```

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus rattus
US-09-915-181A-4

Query Match      77.9%; Score 2313.5; DB 9; Length 582;
Best Local Similarity 79.3%; Pred. No. 2.3e-199;
Matches 428; Conservative 57; Mismatches 50; Indels 5; Gaps 2;

Qy 5 QEEPRKLAGRALGKHLLEKROGAETLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 KEGIKNFAGSLGQIYRVLEKKQNRRETIETEDGKPLEVPEKKAPLDCDCTCFGLPRRYI 72
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 65 IAIMSGLGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVQKAFSMDPETHVLIHGSFF 124
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 IAIMSGLGFCISFGIRCNLGVAIYVMVNNSTTHRGHVVQKAFSMDPETHVLIHGSFF 132
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 125 WGYIVTQIPGGFIQCKFAANRVFGFAIVATSTLNLIPSAARVHYGCVIFVRILQGLVEG 184
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 WGYIITQIPGGYIASRLAANRVFGAAILLSTLNLIPSAARVHYGCVIFVRILQGLVEG 192
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 185 VTPACHGINSKWAPPLERSRLATTAFCGSYAGAVVAMPAGVLVQYSGMSSVFVYVGSF 244
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 193 VTPACHGINSKWAPPLERSRLATTSFCGSYAGAVIAMPLAGILVQYTGWSSVFVYVGSF 252
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 245 GIFWYLFLLVSVESPALHPSISEERKYIEDAIGESAKLNPITKFTSPWRRFFTSMPV 304
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 253 GWMYMFLLVSVESPAKHTITDEERYIEESIGESANLLGAMKEKFTPKRKEFTSMPV 312
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 YAIIVANFCRSWTYLLISOPDYFEEVFGFEISKVGLVLSALPHLVMITIIPIGGQIADF 364
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 313 YAIIVANFCRSWTYLLISOPDYFEEVFGFEISKVGLVLSALPHLVMITIIPIGGQIADF 372
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 365 LRSRRIMSTTVNRKLMNCGFGMEATLLLVVGYSHSKGVAISFLVLAVGSGFAISGFNV 424
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 373 LRSQKILSTTVRKIMNCGFGMEATLLLVVGYSHTRGVASFLVLAVGSGFAISGFNV 432
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 425 NHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHYGGVI 484
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 433 NHLDIAPRYASILMGISNGVGTLSGMVCPPIIVGAMTKHKTREEQYVFLIASLVHYGGVI 492
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 485 FYGVFASGEKOPWAEPEEMSEKCGFVGHDLAGSDDEMEDEAEPPCAPPPSYGAT 544
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 493 FYALFASGEKQPWADPEETSEKCGFIHEDEL----DEETGDTIQ-NVINYGTTSYGAT 547

RESULT 9
US-10-205-331-7
; Sequence 7, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brookesbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Differentiation-associated Na-dependent inorganic phosphate cotra
US-10-205-331-7

```

```
Query Match      77.9%; Score 2313.5; DB 15; Length 582;
Best Local Similarity 79.3%; Pred. No. 2.3e-199;
Matches 428; Conservative 57; Mismatches 50; Indels 5; Gaps 2;

QY 5 QEEFKLAGRALGKHLRLEKQEGAEATLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
DB 13 KEGIKNFAGKSGQIYRVLEKQDNRETIETLEDGKPEVPKCAPLDCDCTCFGLPRRYI 72
QY 65 IAIMSGLGFCISFGIRCNLGVVAIVSMVNNSTHRRGHVVVQKAOFSWDPETVGLIHGSPF 124
DB 73 IAIMSGLGFCISFGIRCNLGVVAIVDMVNNSTHRRGKVIERKAKFNWDPETVGLIHGSPF 132
QY 125 WGYIVTQIPGGFICOKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
DB 133 WGYIITQIPGGYIASRLAANRVFGAAILLTSTLNMLIPSAARVHYGCVIFVRILQGLVEG 192
QY 185 VTPACHGIWSKAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSSVFVYGSF 244
DB 193 VTPACHGIWSKAPPLERSRLATTSFCGSYAGAVIAMPPLAGILVQYTGWSSVFVYGSF 252
QY 245 GIFWYLFWLLVYSYPALHPSISEERKYIEDATGESAKLMNPLTKSTPWRRPFTSPV 304
DB 253 GIWYMFLLVYSYPALHPSISEERKYIEDATGESAKLMNPLTKSTPWRRPFTSPV 312
QY 305 YAIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVLVSALPHLVMITIIVIPIGQIADF 364
DB 313 YAIIVANFCRSWTFYLLISQPAYFEEVFGFEISKVMLSAVPHLVMITIIVIPIGQIADF 372
QY 365 LRSRIMSTTVKLMNCGGFGMEATLLLVGYSHSKGVAISFLVAVFGFSGFAISGRNV 424
DB 373 LRSQILSTTVKLMNCGGFGMEATLLLVGYSHTRGVVAISFLVAVFGFSGFAISGRNV 432
QY 425 NHDIAPRYASILMGISNGVGTLSGMVCPILIVGAMTKHKTREEWQYVFLIASLVHYGVI 484
DB 433 NHDIAPRYASILMGISNGVGTLSGMVCPILIVGAMTKHKTREEWQYVFLIASLVHYGVI 492
QY 485 FYGVFASGEKQWAPPEEEMSEKCGFVGHQDLAGSDDEMEDEAPPPGAPPAPPSYCAT 544
DB 493 FYALFASGEKQWAPPEEEMSEKCGFIHDEL----DEETGDTQ-NVINGYTKSYCAT 547

RESULT 10
US-09-740-041-2
; Sequence 2, Application US/09740041
; Patent No. US20020082190A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001
; CURRENT APPLICATION NUMBER: US/09/740,041
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Human
US-09-740-041-2

Query Match      73.6%; Score 2185; DB 9; Length 589;
Best Local Similarity 76.3%; Pred. No. 8.8e-188;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

QY 5 QEEFKLAGRALGKHLRLEKQEGAEATLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
DB 18 KEGVKNVAGDSGLIQRKIDGTTTEEDNIELNEEGRPVQTSRPSPLCDCHCCGLPKRYI 77
QY 65 IAIMSGLGFCISFGIRCNLGVVAIVSMVNNSTHRRGHVVVQKAOFSWDPETVGLIHGSPF 124
DB 78 IAIMSGLGFCISFGIRCNLGVVAIVDMVNNSTHRRGKVIERKAKFNWDPETVGLIHGSPF 137

Query Match      73.6%; Score 2185; DB 14; Length 589;
Best Local Similarity 76.3%; Pred. No. 8.8e-188;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

QY 5 QEEFKLAGRALGKHLRLEKQEGAEATLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
DB 18 KEGVKNVAGDSGLIQRKIDGTTTEEDNIELNEEGRPVQTSRPSPLCDCHCCGLPKRYI 77
QY 65 IAIMSGLGFCISFGIRCNLGVVAIVSMVNNSTHRRGHVVVQKAOFSWDPETVGLIHGSPF 124
DB 78 IAIMSGLGFCISFGIRCNLGVVAIVDMVNNSTHRRGKVIERKAKFNWDPETVGLIHGSPF 137

Query Match      73.6%; Score 2185; DB 9; Length 589;
Best Local Similarity 76.3%; Pred. No. 8.8e-188;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

QY 5 QEEFKLAGRALGKHLRLEKQEGAEATLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
DB 18 KEGVKNVAGDSGLIQRKIDGTTTEEDNIELNEEGRPVQTSRPSPLCDCHCCGLPKRYI 77
QY 65 IAIMSGLGFCISFGIRCNLGVVAIVSMVNNSTHRRGHVVVQKAOFSWDPETVGLIHGSPF 124
DB 78 IAIMSGLGFCISFGIRCNLGVVAIVDMVNNSTHRRGKVIERKAKFNWDPETVGLIHGSPF 137
```

```
QY 125 WGYIVTQIPGGFICOKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
DB 138 WGYIWTQIPGGFISNKFAANRVFGAAILTSTLNMLIPSAARVHYGCVIQLQGLVEG 197
QY 185 VTPACHGIWSKAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSSVFVYGSF 244
DB 198 VTPACHGIWSKAPPLERSRLATTSFCGSYAGAVVAMPPLAGVLVQYIGWSSVFYIYGMF 257
QY 245 GIFWYLFWLLVYSYPALHPSISEERKYIEDATGESAKLMNPLTKSTPWRRPFTSPV 304
DB 258 GIWYMFLLQAYECPAAHPTISNEEKTYIETISGEGANVVS-LSKFSTPWKRFFTSIPV 316
QY 305 YAIIVANFCRSWTFYLLISQPDYFEEVFGFEISKVLVSALPHLVMITIIVIPIGQIADF 364
DB 317 YAIIVANFCRSWTFYLLISQPAYFEEVFGFEISKVLVSALPHLVMITIIVIPIGQIADF 376
QY 365 LRSRIMSTTVKLMNCGGFGMEATLLLVGYSHSKGVAISFLVAVFGFSGFAISGRNV 424
DB 377 LRSQILSTTVKLMNCGGFGMEATLLLVGYSHTRGVVAISFLVAVFGFSGFAISGRNV 436
QY 425 NHDIAPRYASILMGISNGVGTLSGMVCPILIVGAMTKHKTREEWQYVFLIASLVHYGVI 484
DB 437 NHDIAPRYASILMGISNGVGTLSGMVCPILIVGAMTKHKTREEWQYVFLIASLVHYGVI 496
QY 485 FYGVFASGEKQWAPPEEEMSEKCGFVGHQDLAGSDDEMEDEAPPPGAPPAPPSYCAT 544
DB 497 FYGVFASGEKQWADPENLSEKCGIIDDELA--EEELAHNES---PASPKKMSYCAT 551

RESULT 11
US-10-389-967-2
; Sequence 2, Application US/10389967
; Publication No. US20030166153A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001001-DIV
; CURRENT APPLICATION NUMBER: US/10/389,967
; CURRENT FILING DATE: 2003-03-18
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-389-967-2

Query Match      73.6%; Score 2185; DB 14; Length 589;
Best Local Similarity 76.3%; Pred. No. 8.8e-188;
Matches 412; Conservative 53; Mismatches 69; Indels 6; Gaps 3;

QY 5 QEEFKLAGRALGKHLRLEKQEGAEATLELSADGRPVTTQTRDPVVDCTCFGLPRRYI 64
DB 18 KEGVKNVAGDSGLIQRKIDGTTTEEDNIELNEEGRPVQTSRPSPLCDCHCCGLPKRYI 77
QY 65 IAIMSGLGFCISFGIRCNLGVVAIVSMVNNSTHRRGHVVVQKAOFSWDPETVGLIHGSPF 124
DB 78 IAIMSGLGFCISFGIRCNLGVVAIVDMVNNSTHRRGKVIERKAKFNWDPETVGLIHGSPF 137
QY 125 WGYIVTQIPGGFICOKFAANRVFGFAIVATSTLNMLIPSAARVHYGCVIFVRILQGLVEG 184
DB 138 WGYIWTQIPGGFISNKFAANRVFGAAILTSTLNMLIPSAARVHYGCVIQLQGLVEG 197
QY 185 VTPACHGIWSKAPPLERSRLATTAFCGSYAGAVVAMPPLAGVLVQYSGWSSVFVYGSF 244
DB 198 VTPACHGIWSKAPPLERSRLATTSFCGSYAGAVVAMPPLAGVLVQYIGWSSVFYIYGMF 257
QY 245 GIFWYLFWLLVYSYPALHPSISEERKYIEDATGESAKLMNPLTKSTPWRRPFTSPV 304
DB 258 GIWYMFLLQAYECPAAHPTISNEEKTYIETISGEGANVVS-LSKFSTPWKRFFTSIPV 316
```

Qy 305 YAIIVANFCRSWTFYLLIIISQPDYFEEVFGFEISKVGLVLSALPHLVMTIIVPIGGIADF 364
Db 317 YAIIVANFCRSWTFYLLIIISQPAYFEEVFGFAISKVGLLSAAPHVMVTIIVPIGGIADY 376
Qy 365 LRSRIMSTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLAVLAVGSGFAISGFNV 424
Db 377 LRSRQIITTTAVRKIMNCGGFGMEATLLLVVGFSGTKGVAISFLVLAFLVAVGSGFAISGFNV 436
Qy 425 NHLDIAPRYASILMISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVH 484
Db 437 NHLDIAPRYASILMISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVH 496
Qy 485 FYGVFASGEKQWAPPEMSEKCGFVGHQDLAGSDSEMEDEAEPPGAPPAPP 544
Db 497 FYGVFASGEKQWADPENLSEKCGIIDQDELA--EEIELNHE--FASPKKMSYGAT 551

RESULT 12
US-09-915-181A-3
; Sequence 3, Application US/09915181A
; Patent No. US2002098473A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ROBERT
; APPLICANT: BELLOCCHIO, ELIZABETH
; APPLICANT: FREMEAUX, ROBERT
; APPLICANT: REIMER, RICHARD
; TITLE OF INVENTION: NOVEL GLUTAMATE TRANSPORTERS
; FILE REFERENCE: 305T-932610US
; CURRENT APPLICATION NUMBER: US/09/915.181A
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/220,556
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 850
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-181A-3

Query Match 73.2%; Score 2174.5; DB 9; Length 850;
Best Local Similarity 76.0%; Pred. No. 1.3e-186;
Matches 414; Conservative 51; Mismatches 69; Indels 11; Gaps 5;

Qy 5 QEEPRKLAGALGKHLLEKROGAETLELSADGRPVTTOTRPPVVDCTCGLPRIYI 64
Db 26 KEGVNAVGSGLQLRKLDGTNEEGDAIESEBGRPVQTSRARAPVDCSCGIPKRYI 85
Qy 65 IAIMSGLGFCISFGIRCNLGVAIIVSMVNNSTTHRGHVWVQKQAFSWDPETVG---LIH 120
Db 86 IAVMSGLGFCISFGIRCNLGVAIIVSMVNNSTVYDGPKEIQTAQFNWDPETVGRANSLIH 145
Qy 121 GSPFWGIVTQIPGGTICQKPAANRVFGAIVATSTLNLIPSAAARVHYGVIVRILQG 180
Db 146 GSPFWGIVTQIPGGTISNKAANRVFGAIIFTSTLNLMTIPSAAARVHYGVCMVIRLQG 205
Qy 181 LVEGVTPACHGINSKAPPLERSRLATTAFCSYAGAVAMPLAGVLVOYSGHSSVFYV 240
Db 206 LVEGVTPACHGINSKAPPLERSRLATTAFCSYAGAVAMPLAGVLVOYIGWASAFYI 265
Qy 241 YGSPGIFWYLFLLIV-SYEGPALHPSISEERKVIIEAIGESAKLMNPLTKFSTPWRFF 299
Db 266 YGMEGIIWYFWLLQLQAYCEPAVHTIENERTIETISGEGANLAS-LSKFNTPWRFF 324
Qy 300 TSMFYVIAIIVANFCRSWTFYLLIIISQPDYFEEVFGFEISKVGLVLSALPHLVMTIIVPIGG 359
Db 325 TSLPVYIAIIVANFCRSWTFYLLIIISQPAYFEEVFGFAISKVGLLSAAPHVMVTIIVPIGG 384
Qy 360 QIADFLSRIMSTNVRKLMNCGGFGMEATLLLVVGYSHSKGVAISFLVLAFLVAVGSGFAI 419
Db 385 QLADYLSRKILATTTAVRKIMNCGGFGMEATLLLVVGFSGTKGVAISFLVLAFLVAVGSGFAI 444

Qy 420 SGFNVHLDIAPRYASILMISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVH 479
Db 445 SGFNVHLDIAPRYASILMISNGVGTLSGMVCPPIIVGAMTKHKTRREWQYVFLIASLVH 504
Qy 480 YGGVIFVGFASGEKQWAPPEMSEKCGFVGHQDLAGSDSEMEDEAEPPGAPPAPP 539
Db 505 YGGVIFVGFASGEKQWADPENLSEKCGIIDQDELA--EETELNHEA---FVSPRKKM 559
Qy 540 SYGAT 544
Db 560 SYGAT 564

RESULT 13
US-10-287-226-300
; Sequence 300, Application US/10287226
; Publication No. US20040086875A1
; GENERAL INFORMATION:
; APPLICANT: Agee, Michele L.,
; APPLICANT: Alsobrook, John P.,
; APPLICANT: Berghs, Constance,
; APPLICANT: Boldog, Ference,
; APPLICANT: Burgess, Catherine E.,
; APPLICANT: Chant, John S.,
; APPLICANT: Chaudhuri, Amitabha,
; APPLICANT: DiPippo, Vincent A.,
; APPLICANT: Edinger, Shlomit R.,
; APPLICANT: Eisen, Andrew,
; APPLICANT: Ellerman, Karen,
; APPLICANT: Gangolli, Esha A.,
; APPLICANT: Gorman, Linda,
; APPLICANT: Gerlach, Valerie,
; APPLICANT: Ji, Weizhen,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Khrantsov, Nikolai,
; APPLICANT: Li, Li,
; APPLICANT: Malyankar, Uriel M.,
; APPLICANT: MacDougall, John R.,
; APPLICANT: Mezes, Peter S.,
; APPLICANT: Miller, Charles E.,
; APPLICANT: Millet, Isabelle,
; APPLICANT: Ooi, Chean Eng,
; APPLICANT: Ort, Tatiana,
; APPLICANT: Padigaru, Muralidhara,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rastelli, Luca,
; APPLICANT: Rieger, Daniel K.,
; APPLICANT: Rothenberg, Mark E.,
; APPLICANT: Shenoy, Suresh G.,
; APPLICANT: Spaderna, Steven K.,
; APPLICANT: Spytek, Kimberley A.,
; APPLICANT: Taupier, Jr., Raymond J.,
; APPLICANT: Verniet, Corine A.M.,
; APPLICANT: Zerhusen, Bryan D.,
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-480C
; CURRENT APPLICATION NUMBER: US/10/287,226
; CURRENT FILING DATE: 2002-11-04
; PRIOR APPLICATION NUMBER: 60/334,421
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,392
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/360,148
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04

US-10-369-493-5823

Query Match	43.7%	Score 1297;	DB 15;	Length 576;
Best Local Similarity	47.7%	Pred. No. 9.2e-108;		
Matches 262;	Conservative 88;	Mismatches 171;	Indels 28;	Gaps 10;

Qy	9	RKLGRALGKLRLLERKQGAETLELSADGRPVTTQTRDP---	PVVDCTCFGLPR-RYI	64
Db	12	KOMVGEPLAKVTAAASATGAPQOMQOEENENPMQMSHKNKLVQVMEQTWIGKCRKRWL		71
Qy	65	IAIMSGLGFCISFGIRCNLGVAVISWVNNSTHRRGHVVQKQAFSDNDPVTGLIHGSFF		124
Db	72	LAILANWGFMSFGIRCNFGAKTHMYKNYTDYPG---KVMHEFNWTTIDELSVNESSIF		128
Qy	125	WGYIVTQIPGGFICOKFAANRVFGFAIVATSTLNMIPSAAARVHYG-CVIEVRILQGLVE		183
Db	129	YGYLVTTQIPAGFLAAPPNNKLFPGFIVGGAFLNLLPYGFKVSDYLVAFIQTQGLVQ		188
Qy	184	GVTYPACHGINSKWAPPLERSRLATTAPCGSYAGAVVAMPPLAGVLVQYSGWSSVYVYGS		243
Db	189	GVCYPAMHGVWRYWAPPMERSKLATTFTGYSAGAVLGLPLSAFLVSVSWAAPFYLYGV		248
Qy	244	FGIFWYLFWLIVSVESPALHPSISEERKVIYEDAIAGESAKLMNPLTKFSTPWRFFTSMP		303
Db	249	CGVIWAILWFCVTPEKPAFHTISQEEKIFIEDAIGHVSN-THPTIR-SIPWKAIVTSKP		306
Qy	304	VYAIIVANFCRSWTFYLLLI SQPDYFBEVFGFEISKVLVSALPHLVMTIIVPIGGQIAD		363
Db	307	VWAIIVANFARSWTFYLLLNQLTYMKEALGMKIADSGLLAAIHPHVMGCVVLMGGQLAD		366
Qy	364	PLRRRIMSTTVNKRKLMNCGGFGMEATLLLVGYSHSKGVAISFLVLAVGFSGFAISGFN		423
Db	367	YLRNKLILSTAVRKIFNCGGFGGEAAFMILIVATTSDDTAIMALIAAVGMSGFAISGFN		426
Qy	424	VNHLDIAPRYASIIIMGLSNGVGTLSGMVCPPIIVGAMTKHKTREWQVVELIASLVHYGV		483
Db	427	VNHLDIAPRYAAIIMGFSNGIGTLAGLTCPPVTEAFTAH-SKHGWTSVFLLASLIHFTGV		485
Qy	484	IFYGVFASGEKQPAEPEEMSE-----EKCGFVG-----HDQLAGSDDSEMEDE		527
Db	486	TFYAVYASGELQEWAEPEKEEBEWSNKNLVNKTNGINGYGAETTTQLPAGVDSYQAQ		545
Qy	528	ABP-PGAPP 535		
Db	546	AAPAGTNP 554		

Search completed: June 2, 2005, 11:44:28
Job time : 142 secs

THIS PAGE BLANK (USPTO)
THIS PAGE BLANK (USPTO)